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First Named Inventor or Application Identifier Raymond J. Dattwyler

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Title of Invention

Groups of Borrelia Burgdorferi And Borrelia Afzelii That Cause Lyme Disease In Humans

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO: Assistant Commissioner for Patents
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1. Fee Transmittal Form
(Submit an original, and a duplicate for fee processing)
2. Specification **[Total Pages [55]]**
(preferred arrangement set forth below)
 - Descriptive title of the invention
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 - Reference to microfiche Appendix
 - Background of the Invention
 - Summary of the Invention
 - Brief Description of the Drawings
 - Detailed Description
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 - Abstract of the Disclosure
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**GROUPS OF *BORRELIA BURGDORFERI* AND *BORRELIA AFZELII*
THAT CAUSE LYME DISEASE IN HUMANS**

RELATED APPLICATIONS

- This application claims the benefit of U.S. Provisional Application No.
5 60/140,042, filed June 18, 1999, the entire teachings of which are incorporated herein
by reference in their entirety.

GOVERNMENT SUPPORT

- The invention was supported, in whole or in part, by grant AIAR37256 from
The National Institutes of Health, grant RO1AI33454 from the National Institute of
10 Infectious Disease and cooperative agreement number U50/CCU210518 from the
Centers for Disease Control. The Government has certain rights in the invention.

BACKGROUND OF THE INVENTION

- Lyme disease begins at the site of a tick bite, producing a primary infection with
spread of the organism to secondary sites occurring early in the course of infection.
15 Lyme disease is a progressive multi-system disorder and is the most common vector-
borne disease in both North America and Europe. This disease was first described as a
focus of pediatric arthritis patients in Old Lyme, CT (Steere, A.C., *et al.*, *Arth. Rheum.*

20:17 (1977)). The association of this syndrome with the bite of the deer tick, *Ixodes scapularis*, led to the identification of the spirochete *Borrelia burgdorferi* as the causative agent (Burgdorfer, W., et al., *Science*, 216:1317-1319 (1982)). As culture isolation of the bacterium from clinical and field samples became more efficient,

- 5 Baranton and colleagues described three pathogenic genospecies, *B. Burgdorferi* sensu stricto (*B. Burgdorferi* or *B.b.s.s.*), *B. afzelii*, and *B. garinii* (Baraton, G., et al., *Int. J. Syst. Bacteriol.* 42:378-383 (1992)). These are members of a species complex, *B. burgdorferi* sensu lato, which consists of at least 10 different genospecies (Piken, R.N., et al., *J. Invest. Dermatol.*, 110:211-214 (1998); Postic, D., et al., *Int. J. Syst. Bacteriol.* 10: 44:743-752 (1994); Valsangiacomo, C.T., et al., *Int. J. Syst. Bacteriol.* 47:1-10 (1997)).
- 10 *B. Burgdorferi*, *B. afzelii* and *B. garinii* are thought to be pathogenic and all are found in Europe, but in North America, *B. burgdorferi* is the only pathogenic genospecies found. Each of these three genospecies is associated with distinct clinical manifestations (Van Dam, A. P. et al., *Clin. Infect. Dis.* 17:708-717 (1993)). This implies that differences in
- 15 genospecies may play an important role in the wide array of clinical manifestations observed in Lyme Disease.

As an infected tick begins to feed on a mammal, the synthesis of outer surface protein C (OspC) is induced (Schwan, T.G., et al., *Proc. Natl. Acad. Sci.* 92:2909-2913 (1995)). Thus, in early infection, OspC is the major outer membrane protein expressed by the spirochete (Fung, B.P., et al., *Infect. Immun.* 62:3213-3221 (1994); Padula, S.J., et al., *J. Clin. Microbiol.*, 32:1733-1738 (1994)). Even though OspC has been demonstrated to have limited surface exposure (Cox, D.L., et al., *Proc. Natl. Acad. Sci.*, 93:7973-7978 (1996); Mathiesen, M. M., et al., *Infect Immun.* 66:4073-4079 (1998)), OspC is a potent immunogen. Immunization with OspC is protective against tick-transmitted *Borrelia* infection (Gilmore Jr., R.D., *Infect Immun.* 64:2234-2239 (1999)). However, because OspC is highly variable in its sequence, the protection is limited to the *Borrelia burgdorferi* strain expressing the same immunizing OspC encoded by a specific allele. Challenge with heterologous isolates, expressing other *ospC* alleles

results in infection (Probert, W.S., *et al.*, *J. Infect. D.*, 175:400-405 (1997)). OspC is very diverse (Jauris-Heipke, S., *et al.*, *Med. Microbiol. Immunol.* 182:37-50 (1993)). Livey *et al.* found thirty-four alleles in seventy-six *B. burgdorferi sensu lato* isolates (Livey, I., *et al.*, *Mol. Microbiol.* 18:257-269 (1995)).

5 Currently, Lyme Disease is treated with antibiotics. However, such treatment is not always successful in clearing the infection. Treatment is often delayed due to improper diagnosis with the deleterious effect that the infection proceeds to a chronic condition, where treatment with antibiotics is often not useful. One of the factors contributing to delayed treatment is the lack of effective diagnostic tools. W

10 Furthermore, while antigens such as OspC are known to be protective, in some cases the existence of multiple alleles of these antigens greatly hinders the development of vaccines based on such antigens that would protect against more than one strain of *Borrelia*. Two independent trials of first generation vaccines for the prevention of Lyme disease, recently studied the efficacy and safety of a vaccine that is based on 15 recombinant outer surface protein A (OspA) (Sigal, L.H. *et al.*, *N. Engl. J. Med.* 339:216-222, 1998; Steere, A.C. *et al.*, *N. Engl. J. Med.* 339:209-215, (1998)). However, a vaccine that consists of recombinant OspA may require frequent booster immunizations. Natural infection with *B. burgdorferi* does not elicit an antibody response to OspA, as it does against OspC. What is needed is a selection of *Borrelia* 20 antigens that can be used to either diagnose or vaccinate against all or most forms of *Borrelia* that cause systemic disease.

Differences in the frequency of *B. burgdorferi*, *B. garinii*, and *B. afzelii* in ticks and human infection has lead to the hypothesis that the different genospecies are differentially pathogenic (Picken, R.N. *et al.*, *J. Invest. Dermatol.* 110:211-214, 1998; 25 Van Dam, A.P. *et al.*, *Clin. Infect. Dis.* 17:708-717, 1993). Nevertheless, the number of different strains within a given genospecies and the differences between the strains of a given genospecies as well as between genospecies impose obstacles in the development of immunogenic protein compounds for use as diagnostic and vaccine agents in the

detection, prevention and treatment of Lyme disease. A number of investigators have used OspC as a serodiagnostic antigen for early Lyme disease (Fung, B.P. *et al.*, *Infect. Immun.* 62:3213-3221, 1994; Gerber, M.A. *et al.*, *J. Infect. Dis.* 171:724-727, 1995; Padula, S.J. *et al.*, *J. Clin. Microbiol.* 32:1733-1738, (1994)). In these tests, the use of 5 OspC as a diagnostic antigen gave highly specific, but not sensitive results. However, these studies included only one *B. burgdorferi* strain and therefore only one type of OspC. Routine tests for the diagnosis of Lyme disease also use a single strain protocol and therefore a single OspC allele for detection of antibody to the spirochete. It is not clear what mixture of OspC proteins must be used to make useful diagnostic and 10 vaccine tools, effective against more than one Lyme disease causing strains of *Borrelia*, if not against most if not all of the invasive strains within a genospecies. Preferably, such a mixture would be effective against all invasive strains of Lyme disease *causing borrelia*.

SUMMARY OF THE INVENTION

15 The present invention is drawn to a composition comprising OspC polypeptides from Lyme Disease causing *Borrelia*. In one embodiment, the composition of the present invention comprises an OspC polypeptide or fragment thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of A, B, I and K, excepting the combination consisting of two OspC proteins, wherein one OspC protein 20 is from OspC family A and the second OspC protein is from OspC family I. In another embodiment, the composition of the present invention comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B.

The present invention is also drawn to a method of immunizing an animal against Lyme disease, comprising administering a composition comprising OspC 25 polypeptides from Lyme Disease causing *Borrelia*. In one embodiment of the present invention, the composition comprises a OspC polypeptide or fragment thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A,

B, I and K, excepting the combination consisting of two OspC proteins, wherein one OspC protein is from OspC family A and the second OspC protein is from OspC family I. In another embodiment of the present invention, the composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families 5 A and B. The composition of the present invention together with suitable excipients and/or adjuvants is administered to an animal such that the animal develops an immune response to at least one OspC polypeptide of the composition.

The present invention is also drawn to a method of detecting an immune response to Lyme Disease causing *Borrelia* in a host sample. The method comprises 10 contacting a host sample with a composition comprising OspC polypeptides from Lyme disease causing strains of *Borrelia*, such that anti-OspC antibodies, if present, in said sample bind to said OspC polypeptides. In one embodiment, the composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia burgdorferi* OspC families A, B, I and K. The amount of antibodies that have bound said OspC 15 polypeptides or fragments thereof are measured; thereby detecting an immune response to Lyme disease causing *Borrelia*.

The present invention is also drawn to a diagnostic kit comprising OspC polypeptides from Lyme Disease causing *Borrelia*. In one embodiment of the present invention, the diagnostic kit comprises at least one OspC polypeptide or diagnostic 20 fragment thereof from each of *Borrelia burgdorferi* OspC families A, B, I and K. In another embodiment of the present invention, the diagnostic composition comprises at least one OspC polypeptide or diagnostic fragment thereof from each of *Borrelia afzelii* OspC families A and B.

In other embodiments of the present invention, the composition comprises at 25 least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B. In still other embodiments, the composition comprises OspC polypeptides or fragments thereof from *Borrelia burgdorferi*, *Borrelia afzelii*, *Borrelia garinii* and combinations thereof.

The present invention is also drawn to chimeric proteins for use in the methods of the present invention. In one embodiment, the present invention is drawn to a chimeric protein comprising OspC polypeptides from two or more OspC families of Lyme Disease causing *Borrelia*. In one embodiment, the families comprise *Borrelia burgdorferi* OspC families A, B, I and K. In other embodiment, the families comprise *Borrelia afzelii* OspC families A and B. In still other embodiments, the composition comprises chimeric OspC polypeptides or fragments thereof from *Borrelia burgdorferi*, *Borrelia afzelii*, *Borrelia garinii* and combinations thereof.

The chimeric proteins of the present invention comprise at least a first and a second polypeptide of OspC, such that the first polypeptide comprises OspC from about base 26 to about base 630 of a first *ospC* gene and the second polypeptide comprises about base 28 to about base 570 of a second *ospC* gene. The chimeric proteins of the present invention can be used in the immunization and detection methods of the present invention.

The present invention provides the minimum number of *Borrelia burgdorferi* and *Borrelia afzelii* families that are responsible for systemic disease in humans and is useful for vaccines and diagnostic kits. The present invention provides a combination of proteins that, when used as a vaccine, prevent Lyme disease from becoming systemic. The proteins and chimeric proteins of the present invention can be effective in preventing of Lyme disease as well as having a therapeutic effect on established infection, for example after the tick bite is noticed by the patient. The proteins and chimeric proteins of the present invention are expected to act at the level of the tick as well as the level of the host in preventing both infection and disease due to *Borrelia burgdorferi*, *Borrelia afzelii* and/or *Borrelia garinii*. The present invention allows the development of a worldwide vaccine comprising only six proteins necessary to generate a protective immune response against all pathogenic strains of *Borrelia burgdorferi* and *Borrelia afzelii*.

The present invention also provides improved diagnostic tools. Because of the present invention, it is now possible to prepare diagnostic tools comprising OspC antigens representing the four pathogenic families of *Borrelia burgdorferi* and/or the two pathogenic families of *Borrelia afzelii*, thereby detecting clinically important 5 exposure to pathogenic bacteria while overlooking the remainder of the families which do not cause pathogenic disease.

As demonstrated herein, a significant proportion, if not all, systemic *B. burgdorferi* sensu stricto infections in humans are associated with four *ospC* groups and that a significant portion, if not all, systematic *B. afzelii* infections in humans are 10 associated with two *ospC* groups. Vaccines against OspC are known to be protective, but have been limited by the diversity of *ospC* (Probert, W.S. et al., *J. Infect. D.* 175:400-405, (1997)). The polypeptides of the present invention provide immunogenic proteins, fragments and chimeric proteins thereof for highly protective vaccines and diagnostics. The present invention provides a vaccine that includes one or more of 15 these four forms of OspC. The vaccines of the present invention should be an important second level of protection against disseminated infection of the *B. burgdorferi* spirochete. Furthermore, single-stranded conformational polymorphism (SSCP) analysis described herein may provide a rapid and powerful tool to monitor vaccine efficacy by detecting rare or new invasive *ospC* groups.

20 New diagnostic assays of the present invention, based on major *ospC* groups A, B, I, and K are useful to identify those at risk for progressive illness. Given that OspC proteins are antigenically variable, individuals infected with one strain may produce an antibody response that is not reactive with an OspC protein from a different major group. Antibody detection using antigen preparations of the present invention, 25 incorporating a proper mix of invasive clones of *B. burgdorferi* will be much more sensitive than the present, single strain protocols. The compositions of the present invention not only elicit humoral and cell mediated immune responses, the

compositions of the present invention are also capable of detecting both humoral and cell mediated immune response when used to test a host sample.

The present invention provides both lipidated OspC polypeptides, fragments thereof and chimeric proteins comprising two or more OspC polypeptides, wherein the 5 chimeric protein has a lipidation signal, such as the lipidation signal from outer surface protein B at the 5' terminus of the gene encoding the chimera. Furthermore, the present invention provides unlipidated OspC polypeptides, fragments thereof and chimeric proteins comprising two or more OspC polypeptides, wherein the gene encoding the chimeric protein does not comprise a lipidation signal and the chimeric protein is not 10 lipidated. Unlipidated OspC polypeptides, fragments thereof and chimeric proteins thereof are advantageous due to simpler production methods, improved yields of protein and simpler purification. The unlipidated chimeric proteins of the present invention unexpectedly elicit an immune response against Lyme disease causing strains of *Borrelia* at least as broadly reactive as lipidated OspC proteins that are used as a 15 positive control. Furthermore, the unlipidated OspC chimeric proteins of the present invention elicit an immune response to more than one genospecies of Lyme disease causing strains of *Borrelia*, including genospecies and strains that are not used to generate the chimeric OspC immunogen.

BRIEF DESCRIPTION OF THE DRAWINGS

20 Figure 1 is a schematic diagram of the frequency distribution of major *ospC* groups among *B. burgdorferi* isolates from Eastern Long Island *Ixodes scapularis* ticks.

Figure 2 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or recombinant chimeric *Borrelia* protein (X-axis) against the indicated OspC antigens (legend) where the serum is from the first bleed.

25 Figure 3 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or recombinant chimeric *Borrelia* protein (X-axis) against the indicated OspC antigens (legend) where the serum is from the second bleed.

Figure 4 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia burgdorferi* sensu stricto (legend).

Figure 5 is a bar graph showing the reactivity of serum from mice immunized
5 with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia burgdorferi* sensu lato (legend).

Figure 6 is bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia afzelii* (legend).

10 Figure 7 is bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia garinii* (legend).

Figure 8 is a Table comparing the reactivity of lipidated OspC proteins C1 and
C2 against sera from patients with the indicated condition with the reactivity of the
15 unlipidated chimeric proteins of the present invention, where the number in parentheses
is the total number of sera tested in that category.

DETAILED DESCRIPTION OF THE INVENTION

As described herein, initially nineteen groups of *ospC* from *B. burgdorferi* sensu stricto were found within a small tick population (Wang, I-N., et al., *Genetics*,
20 151:15-30 (1999)). Major *ospC* groups were defined using the observation that *ospC* alleles are either very similar, having less than 2% sequence divergence, or very different, having greater than 8% sequence divergence, with most having greater than 14% sequence divergence.

Based on sequence divergences, alleles of *ospC* can be grouped into twenty-one
25 major groups (Table II). To assess whether strain differences as defined by a given *ospC* group are linked to invasiveness and pathogenicity, the frequency distributions of major *ospC* groups from ticks, from the primary erythema migrans (EM) skin lesion,

and from secondary sites, principally from blood and spinal fluid, were compared. As described herein, the frequency distribution of *ospC* groups from ticks is significantly different from that of primary site infection which in turn is significantly different from secondary sites. The major *ospC* groups A, B, I and K increased in frequency from 5 ticks to the primary site and were the only groups found in secondary sites of the infection. Therefore, three categories of major *ospC* groups are defined herein. One category is common in ticks but very rarely, if ever, causes human disease, a second category that causes only local infection at the tick bite site, and a third category that causes systemic or disseminated disease. While many *ospC* groups found in ticks were 10 also found in primary skin lesions, the frequency distributions are significantly different between ticks and primary skin lesions (Table III). All *ospC* groups were found more or less commonly in ticks. However, only four groups are commonly found in skin lesions or secondary infections (Tables III and IV). As described herein, the primary skin 15 lesions harbored *Borrelia* having *ospC* groups other than A, B, I or K rarely or not at all. More importantly, only these four *ospC* groups were found in secondary sites. The finding that all systemic *B. burgdorferi* sensu stricto infections are associated with four *ospC* groups has importance in the diagnosis, treatment and prevention of Lyme disease.

There is evidence that *ospC* has been transferred between strains and even 20 between genospecies (Wang I-N, *et al.*, *Genetics*, 151:15-30 (1998)). This is not true of *Borrelia* chromosomal genes (Dykhuizen, D.E., *et al.*, *Proc. Natl. Acad. Sci.*, 30:10163-10167 (1999); Maynard Smith, J. and Smith, N.H., *Mol. Biol. Evol.*, 15:590-599 (1998)). However, *ospA* and *ospC* alleles in *B. Burgdorferi* sensu stricto are almost completely linked (Wang I-N, *et al.*, *Genetics*, 151:15-30 (1999)). This suggests that once an *ospC* allele has been transferred into a particular background, there is little or 25 no selection for another similar recombination event. Thus, each major *ospC* group represents a clonal population descended from a single recombination.

Twenty percent of untreated erythema migrans clear spontaneously without causing any systemic complications (Steere, A.C. *et al.*, *Arth. Rheum.* 20:7-17, (1977)).

As demonstrated herein, this is not significantly different ($p = 0.25$ for a 2 by 2 contingency test with double dichotomy) from the percent of non-invasive strains found in the skin, suggesting that the erythema migrans that clear spontaneously are caused by non-invasive clones.

5 There is extensive genetic and antigenic diversity of *ospC* in all three pathogenic genospecies of *B. burgdorferi* sensu lato (Livey, I. et al., *Mol. Microbiol.* 18:257-269, 1995; Masuzawa, T. et al., *Clin. Diagn. Lab. Immunol.* 4:60-63, 1997; Picken, R.N. et al., *J. Invest. Dermatol.* 110:211-214, 1998; Theisen, M. et al., *J. Clin. Microbiol.* 31:2570-2576, 1993; Wang, I-N. et al., *Genetics* 151:15-30 (1999). As demonstrated
10 herein, only four groups of *ospC* alleles are linked to both infectivity and invasiveness, and that invasiveness is confined to a small number of *ospC* clones. It is clear that the *ospA* and *ospC* alleles are tightly linked even though they are on different plasmids (Wang, I-N. et al., *Genetics* 151:15-30 (1999)). If the invasiveness is caused by allelic variation at another locus, this variation is likely to be tightly linked to the *ospC*
15 variation. Thus, *ospC* is a good marker for human pathogenicity and perhaps its determinator. These findings have important implications not only for our understanding of the pathogenesis of this disease but for its diagnosis and prevention.

Spirochetemia is a transient phenomenon, but is presumably key in seeding secondary skin sites, the heart, joints, and nervous system, where these *Borrelia* cause
20 the secondary and tertiary clinical manifestations of Lyme disease. All four invasive groups of *Borrelia burgdorferi* were found in isolates from blood and CSF. The one joint isolate belonged to group A. However, it can be inferred that groups not found in the blood will not be found in the joints since most if not all dissemination of *Borrelia* to secondary sites is via blood.

25 Normally, model organisms are used as substitutes for experiments on humans. However, this substitution works only as long as the properties of the model organism and of humans are the same for the studied phenomena. The human immune system plays a critical role which is expected to be different from the immune response in

model organisms, particularly the mouse. Humans are accidental and usually dead-end hosts while the mouse is a critical host reservoir. The field of population genetics has developed sound procedures for reaching conclusions from survey data.

The chimeric polypeptides of the present invention elicit specific immune responses to OspC. The chimeric polypeptides also elicit immune response against strains of Lyme disease causing *Borrelia* of the same genospecies as that represented by the chimeric OspC as well as Lyme disease causing *Borrelia* of different genospecies than that represented by the chimeric OspC. The immune response includes humoral responses, secretory responses, cell-mediated responses and combinations thereof in an animal treated with the compositions of the present invention. The compositions of the present invention can include additional components suitable for *in vitro* and *in vivo* use. These additional components include buffers, carrier proteins, adjuvants, preservatives and combinations thereof.

The immunogenic compositions of the present invention can be used to immunize animals including humans. Immunization is understood to elicit specific immunogenic responses as described above. As described herein, an immunogenic response includes responses that result in at least some level of immunity in the treated animal, where the animal was treated with a composition comprising at least one protein or chimeric protein of the present invention. In one embodiment, the treated animal develops immunity against infection by Lyme disease causing *Borrelia*, wherein the chimeric proteins of the present invention elicit responses against *Borrelia burgdorferi*, *Borrelia afzelii* and *Borrelia garinii*.

Immunity, as described herein, is understood to mean the ability of the treated animal to resist infection, to resist systemic infection, to overcome infection such as systemic infection or to overcome infection such as systemic infection more easily or more quickly when compared to non-immunized or non-treated individuals. Immunity can also include an improved ability of the treated individual to sustain an infection with reduced or no clinical symptoms of systemic infection. The individual may be

treated with the chimeric proteins of the present invention either proactively, e.g. once a year or maybe treated after sustaining a tick bite.

For use as a vaccine, the composition of the present invention can include suitable adjuvants, well known in the art, to enhance immunogenicity, potency or half-life of the chimeric proteins in the treated animal. Adjuvants and their use are well known in the art (see for example PCT Publication WO 96/40290, the entire teachings of which are incorporated herein by reference). The composition can be prepared by known methods of preparing vaccines. For example, the OspC proteins or chimeric proteins to be used in the compositions can be isolated and/or purified by known techniques such as by size exclusion chromatography, affinity chromatography, preparative electrophoresis, selective precipitation or combinations thereof. The prepared proteins or chimeric proteins can be mixed with suitable other reagents as described above, where the chimeric protein is at a suitable concentration. The dosage of protein or chimeric protein will vary from one μ g to 500 μ g and depends upon the age, weight and/or physical condition of the animal to be treated. The optimal dosage can be determined by routine optimization techniques, using suitable animal models.

The composition to be used as a vaccine can be administered by any suitable technique. In one embodiment, administration is by injection, e.g. subcutaneous, intramuscular, intravenous, or intra peritoneal injection. In another embodiment, the composition is administered to mucosa, e.g. by exposing nasal mucosa to nose drops containing the proteins of chimeric proteins of the present invention. In another embodiment, the immunogenic composition is administered by oral administration. In another embodiment of the present invention the chimeric proteins are administered by DNA immunization.

Like many outer surface proteins of *Borrelia*, OspC is produced in the *Borrelia* spirochete with 5' lipidation. The chimeric polypeptides of the present invention can be produced in both lipidated and non-lipidated form. In one embodiment, the lipidation signal encoded by the wild type *ospC* is removed from the coding sequence, such that

the gene or chimeric gene encodes a non-lipidated OspC or chimeric OspC polypeptide. In another embodiment of the present invention, the lipidation signal of the wild type *ospC* gene is replaced with the lipidation signal of the *ospB* gene. In this embodiment, a lipidated OspC or OspC chimeric protein is produced.

5 The polypeptides of the present invention can be recombinantly expressed in suitable microbial hosts, wherein said hosts include, but are not limited to, bacterial hosts, such as *E. coli*, fungal hosts *S. cerevisiae*, or cell culture hosts such as mammalian cell culture or insect cell culture.

While the lack of lipidation signal allows for the production of large amounts of
10 OspC proteins and chimeric OspC proteins, the lack of lipidation signal was previously thought to render outer surface proteins of *Borrelia* less or non-immunogenic. However, as described herein, the non lipidated chimeric polypeptides of the present invention unexpectedly elicit as broad an immunogenicity as lipidated OspC protein (Figures 2 and 3) and greater immunogenicity against strains of other genospecies
15 (Figure 5-7) compared to the positive controls, which were lipidated OspC from B31 and lipidated OspC from C12.

The proteins and chimeric proteins of the present invention are also antigenic and therefore useful to detect or diagnose the presence of Lyme disease causing *Borrelia*, especially *Borrelia* from groups capable of causing disseminated symptoms of
20 Lyme disease. As described herein, disseminated symptoms refers to infection outside of the erythema migrans skin lesion, e.g. infection in blood, CNS or synovia. As described herein, antigenic refers to the ability of a compound to bind products of an immune response, such as antibodies, T-cell receptors or both. Such responses can be measured using standard antibody detection assays, such as ELISA or standard T-cell activation assays.
25

The present invention is drawn to compositions comprising OspC polypeptides from Lyme disease causing *Borrelia* and chimeric OspC polypeptides. In one embodiment of the present invention, compositions include one or more OspC

polypeptide or fragment thereof from at least two *Borrelia burgdorferi* *ospC* groups, referred also herein as families, selected from the group consisting of A, B, I and K, excepting the combination consisting of two OspC polypeptides from the A and I families. In another embodiment of the present invention, the compositions of the 5 present invention include at least one OspC polypeptide or fragment thereof from each of *Borrelia burgdorferi* *ospC* families A, B, I and K. In another embodiment, the composition includes at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B. In still another embodiment, the composition includes OspC polypeptides from at least one *Borrelia burgdorferi* OspC group or 10 family member selected from the group consisting of A, B, I and K and at least one *Borrelia afzelii* OspC family member selected from the group consisting of A and B.

As described herein, the *ospC* families of the present invention share about 98% homology at the nucleic acid level between strains of the same family and share no more than about 92% homology at the nucleic acid level between strains of different 15 families. Determination of homology excludes any non-*ospC* sequences. Members of the same *ospC* family have similar antigenic profiles, e.g. elicit immune response against similar strains of Lyme disease causing *Borrelia*. The chimeric proteins of the present invention unexpectedly elicit immune response to Lyme disease causing *Borrelia* of different genospecies than the genospecies from which the component 20 polypeptides were derived. In one embodiment of the present invention, *Borrelia burgdorferi* *ospC* family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, PKA, TXGW and strains of *Borrelia* containing *ospC* allele OC1. In another embodiment of the present invention, *Borrelia burgdorferi* *ospC* family B comprises strains 35B808, 61BV3, BUR, DK7, PB3, ZS7 and strains containing *ospC* alleles OC2 25 and OC3. In still another embodiment of the present invention, *Borrelia burgdorferi* *ospC* family I comprises strains 297, HB19 and strains containing *ospC* allele OC10, wherein strain 297 is characterized by *ospC* of GenBank Accession No. L42893. In still another embodiment of the present invention, *Borrelia burgdorferi* *ospC* family K

comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC* allele OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank Accession No. U08284.

- In another embodiment of the present invention, said compositions comprise an
- 5 OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B. In one embodiment of the present invention, *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, Pko, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB. In another embodiment of the present invention *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 143M. As described above for *Borrelia*
- 10 *burgdorferi* the compositions also include chimeric OspC polypeptides of *Borrelia afzelii* families A and B.

In one embodiment of the present invention, the OspC polypeptide OspC polypeptide is a chimeric OspC comprising at least one OspC protein variable region or portion thereof from at least one *ospC* gene. In one embodiment of the present

15 invention, the OspC polypeptide variable region is encoded by a nucleic acid comprising the 3' two thirds of the *OspC* gene, about nucleotide 150 to about nucleotide 519 of an *ospC* gene (or about codon 50 to about codon 173). In another embodiment of the present invention, said OspC polypeptide variable region is encoded by a nucleic acid wherein the nucleic acid comprises, for example, nucleotide 244 to

20 about nucleotide 519 (or about codon 81 to about codon 173), nucleic acid from about nucleotide 337 to about nucleotide 519 (or about codon 112 to about codon 173), nucleic acid from about nucleotide 418 to about nucleotide 519 (or about codon 139 to about codon 173), nucleic acid from about nucleotide 244 to about nucleotide 418 (or about codon 81 to about codon 139), nucleic acid from about nucleotide 337 to about

25 nucleotide 418 (or about codon 112 to about codon 139), and nucleic acid from about nucleotide 150 to about nucleotide 243 (or about codon 50 to about codon 81) of an *ospC* gene.

In still another embodiment, the chimeric OspC polypeptides of the present invention comprises two or more polypeptides wherein a first polypeptide is from a first *ospC* gene from about nucleotide 26 (or about codon 8) to about nucleotide 630 (or about codon 210). In another embodiment, the first polypeptide is from about 5 nucleotide 28. In another embodiment, the first polypeptide is from about nucleotide 53. In still another embodiment, the first polypeptide is from about nucleotide 55. In another embodiment, the first polypeptide is up to about nucleotide 621 of a first *ospC* gene. In still another embodiment, the first polypeptide is up to about nucleotide 582 of a first *ospC* gene. In still another embodiment, the first polypeptide is up to about 10 nucleotide 576 of a first *ospC* gene.

The chimeric OspC of the present invention further comprises a second polypeptide, wherein the second polypeptide is derived from a second *ospC* gene from about nucleotide 28 (or about codon 9) to about nucleotide 571 (or about codon 190).

It is understood that the polypeptides than comprise the chimeric polypeptide 15 can include extra nucleotides or fewer nucleotides from the given *ospC* gene from which the polypeptide is derived in order to simplify the construction of the gene encoding the chimeric polypeptide, e.g. to allow for the use of convenient restriction endonuclease sites or to allow the ligation of the gene fragments such that a contiguous coding region is created. Based on the guidance provided herein, one of ordinary skill 20 in the art would readily be able to add or remove nucleotides from the termini of the gene fragments encoding the polypeptides of the chimeric OspC protein to generate chimeric proteins of the present invention with no or only routine experimentation. Furthermore, there can be an extra about 1 to about 10 amino acids on the N- and/or C-terminus of the polypeptides and chimeric proteins of the present invention and still 25 retain the properties of the present invention.

The present invention also includes variants or altered versions of the OspC polypeptides and nucleic acids encoding said polypeptides. As used herein, a variant of a polynucleotide or polypeptide refers to a molecule that is substantially similar to

- either the entire molecule, or a fragment thereof. For example, when the molecule is a polypeptide, variant refers to an amino acid sequence that is altered by one or more amino acids, wherein either a biological function, structure or antigenicity of said sequence or combination thereof is maintained in the variant. The variant may have
- 5 "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties, *e.g.*, replacement of leucine with isoleucine. Or a variant may have "nonconservative" changes, *e.g.*, replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions, or both.
- Similarly, when the molecule is a polynucleotide, variant refers to a sequence that is
- 10 altered by one or more nucleotides. The variant may have silent variations, wherein the change does not alter the amino acid encoded by the triplet comprising said variation or the variation is not silent, that is, alterations in encoded amino acids are generated.
- As used herein, the term "altered version" refers to a polynucleotide sequence or a polypeptide sequence, wherein said sequence has one or more differences with a
- 15 native or wildtype version of said sequence.
- In another embodiment, the invention includes an isolated nucleic acid molecule comprising a nucleotide sequence which is homologous to one or more of the chimeric sequences of the present invention, or complements thereof. Such a nucleotide sequence exhibits at least about 80% homology, or sequence identity, with one of the
- 20 chimeric OspC sequences, such that the encoded protein retains the antigenicity and immunogenicity of the unaltered chimeric protein. Preferably, the homologous sequences of the present invention shares at least about 90% homology or sequence identity with the corresponding unaltered chimeric *ospC*. Particularly preferred sequences have at least about 95% homology or have essentially the same sequence.
- 25 The altered nucleic acids and homologous nucleic acids of the present invention hybridize to the corresponding chimeric *ospC* under conditions of high stringency. A general description of stringency for hybridization conditions is provided by Ausubel, F.M., *et al.*, *Current Protocols in Molecular Biology*, Greene Publishing Assoc. and

Wiley-Interscience 1987, & Supp. 49, 2000. Factors such as probe length, base composition, percent mismatch between the hybridizing sequences, temperature and ionic strength influence the stability of nucleic acid hybrids. Thus, stringency conditions, sufficient to allow hybridization of oligonucleotides to the template, can be
5 varied by routine optimization to generate high stringency conditions.

Alternatively, conditions for stringency are as described in WO 98/40404, the teachings of which are incorporated herein by reference. In particular, examples of highly stringent, stringent, reduced and least stringent conditions are provided in WO 98/40404 in the Table on page 36. Examples of stringency conditions are shown in
10 Table I below which is from WO98/40404 to Jacobs *et al.*,: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

-20-

Table 1

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
5	A	DNA:DNA	≥ 50 65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	<50 T_B^* ; 1xSSC	T_B^* ; 1xSSC
	C	DNA:RNA	≥ 50 67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	<50 T_D^* ; 1xSSC	T_D^* ; 1xSSC
	E	RNA:RNA	≥ 50 70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	RNA:RNA	<50 T_F^* ; 1xSSC	T_F^* ; 1xSSC
	G	DNA:DNA	≥ 50 65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	<50 T_H^* ; 4xSSC	T_H^* ; 4xSSC
	I	DNA:RNA	≥ 50 67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	<50 T_J^* ; 4xSSC	T_J^* ; 4xSSC
10	K	RNA:RNA	≥ 50 70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	<50 T_L^* ; 2xSSC	T_L^* ; 2xSSC
	M	DNA:DNA	≥ 50 50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	<50 T_N^* ; 6xSSC	T_N^* ; 6xSSC
	O	DNA:RNA	≥ 50 55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
15	P	DNA:RNA	<50 T_P^* ; 6xSSC	T_P^* ; 6xSSC
	Q	RNA:RNA	≥ 50 60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	<50 T_R^* ; 4xSSC	T_R^* ; 4xSSC

[‡]: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and 5 identifying the region or regions of optimal sequence complementarity.

[†]: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length 10 should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log₁₀[Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

15 As used herein, “isolated” refers to nucleic acid or polypeptide that has been removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, polynucleotide or DNA or polypeptide, which is separated from some or all of the coexisting materials in the natural system. An isolated polynucleotide can be part of a vector and/or composition, and still be isolated in that the 20 vector or composition is not part of its natural environment. Likewise polypeptides can be part of a composition and still be isolated in that the composition is not part of its natural environment.

The chimeric proteins of the present invention comprise OspC proteins or polypeptides as described above from two or more OspC families of Lyme disease 25 causing *Borrelia* as described in Table II. In one embodiment of the present invention, said families comprise *Borrelia burgdorferi* OspC families A, B, I and K and *Borrelia afzelii* OspC families A and B. The chimeric proteins of the present invention comprise, for example, a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about codon 18 to about codon 210 of a first *ospC* gene. In another embodiment,

- the sequence is from about codon 8. In another embodiment, the sequence is to about codon 207. In another embodiment, the sequence is to about codon 194. In still another embodiment, the sequence is to about codon 192. The chimeric proteins of the present invention further comprise, for example, a second OspC polypeptide comprising an
- 5 OspC variable polypeptide encoded by nucleic acid fragments as described above. In another embodiment of the present invention, the chimeric protein comprises two or more OspC variable polypeptides as described above.

The chimeric proteins of the present invention further comprise, for example, a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about

10 codon 9 to about codon 190 of a second *ospC* gene.

For the chimeric proteins of the present invention, at least two of said OspC polypeptides or immunogenic fragments thereof are fused together in a single protein, a chimeric protein, encoded by a single nucleic acid, wherein no two adjacent polypeptides in said fusion protein are found in the same configuration in a naturally occurring OspC

15 protein.

In still another embodiment, the OspC proteins or chimeric proteins of the present invention from *Borrelia burgdorferi* and *Borrelia afzelii* are combined in a composition.

The present invention is drawn to a method of detecting an immune response to

20 Lyme Disease causing *Borrelia* in a host sample. The method comprises contacting the host sample with a composition comprising OspC polypeptides from Lyme disease causing strains of *Borrelia*, such that anti-OspC antibodies, if present, in said sample bind to said OspC polypeptides. In one embodiment, the composition comprises one or more OspC polypeptide or diagnostic fragment thereof from two *Borrelia burgdorferi*

25 OspC families selected from the group consisting of A, B, I and K, excluding the composition consisting of two OspC proteins wherein one OspC protein is from OspC family A and the second OspC protein is from OspC family I. The antibodies that bind the OspC polypeptides of the composition are detected or measured; thereby detecting an

immune response to Lyme disease causing *Borrelia*. In another embodiment, the composition comprises at least two *Borrelia* OspC polypeptides or diagnostic fragment thereof from two *Borrelia afzelii* OspC families selected from the group consisting of A and B. In still another embodiment, the composition comprises polypeptides from OspC 5 from *Borrelia burgdorferi* and *Borrelia afzelii*. In still another embodiment, the composition comprises one or more polypeptides from each of *Borrelia burgdorferi* families A, B, I and K and *Borrelia afzelii* families A and B. The composition can also comprise one or more of the chimeric polypeptides of the present invention.

The present invention is also drawn to kits comprising one or more OspC 10 polypeptides or OspC chimeric polypeptides or combinations thereof together with suitable buffers and antibody detection reagents for the detection or diagnosis of Lyme disease causing strain of *Borrelia*. In another embodiment, the kits comprise nucleic acid sufficiently homologous to the OspC polypeptides or OspC chimeric polypeptides to detect nucleic acid encoding *ospC* genes from Lyme disease causing strains of 15 *Borrelia* together with reagents to detect positive hybridization to target DNA or reagents to specifically DNA, for example.

For the purposes of a detection kit, "homologous" refers to two or more sequences that share substantial similarity but are not identical. Two DNA sequences are "substantially similar" when at least about 95% (preferably at least about 98%) of the 20 nucleotides match over a defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc., New York; Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press. For purposes of the present invention, amino acid sequences having, for example, greater than 90 percent similarity are considered substantially homologous.

The vaccine compositions of the present invention elicit humoral and cell mediated immune responses in a host. Furthermore, the diagnostic compositions of the present invention are capable of detecting both humoral and cell mediated immune response from a host sample using standard immunodiagnostic techniques.

5

EXEMPLIFICATION

EXAMPLE 1: - TECHNIQUES

Borrelia strains

One hundred and forty *B. burgdorferi* strains were isolated from primary erythema migrans (EM) lesions, blood or cerebrospinal fluid (CSF) of patients seen at 10 the Lyme Disease Center at Stony Brook, New York, Lyme Disease Diagnostic Center at New York Medical College, Valhalla, New York or the private practices of the two collaborating physicians on the eastern end of Long Island or were obtained from the Centers for Disease Control (CDC). All patients met the Centers for Disease Control surveillance definition for Lyme Disease (CDC, *Morb. Mortal. Wkly. Rep.* 46:20-21, 15 (1997)). Isolates from skin, blood and CSF were obtained using standard techniques (Barbour, A.G., *Yale J. Biol. Med.* 57:521-525, 1984; Berger, B.W. *et al.*, *J. Clin. Microbiol.* 30:359-361, 1992; Wormser, G.P. *et al.*, *J. Clin. Microbiol.* 36:296-298, (1998)). Punch biopsies were taken from the advancing border of the erythema migrans lesion and incubated in BSK-H medium (Sigma, St. Louis, MO) at 34°C to create a 20 culture. There was little culture bias as determined by direct analysis of biopsy tissue compared to culture isolates (Seinost, G. *et al.*, *Arch. Derm.*, 135:1329-1333, (1999)), unlike isolation of *B. burgdorferi* from unfed ticks (Norris, D.E. *et al.*, *J. Clin. Microbiol.* 35:2359-2364, (1997)). In addition, twenty-two *B. burgdorferi* sensu stricto 25 *ospC* sequences were retrieved from GenBank. The tick data used was either from GenBank or from the study of Wang *et al.* (Wang, I-N. *et al.*, *Genetics* 151:15-30 (1999)).

DNA isolation

For isolation of genomic *Borrelia* DNA, log phase cells were harvested by centrifugation at 10,000 RPM for 30 minutes at 4°C. The bacterial pellet was resuspended in Tris/saline-buffer (10 mM Tris (pH 7.5), 150 mM NaCl). The bacteria 5 were then pelleted and resuspended in TNE (10 mM Tris (pH 7.5) 150 mM NaCl, 1 mM EDTA). Freshly prepared lysozyme (20 mg/ml in TNE), sodium dodecyl sulfate (10%) and proteinase K (20 mg/ml) were added and the mixture was incubated at 50°C for one hour, followed by RNase treatment. DNA was extracted with phenol/chloroform, precipitated with ethanol and resuspended in TE buffer.

10 Polymerase chain reaction

The *ospC* gene was amplified using PCR, as described previously (Wang, I-N. *et al.*, *Genetics* 151:15-30 (1999)). The *OspC* gene was amplified using two external primers: 5'-AAA GAA TAC ATT AAG TGC GAT ATT-3' (+), SEQ ID NO: 1, beginning at base 6; and 5'-GGG CTT GTA AGC TCT TTA ACT G-3' (-), SEQ ID NO: 15 4, ending at base 602. The 5' half of *ospC* was amplified using SEQ ID NO: 1 and the reverse primer, 5'-CAA TCC ACT TAA TTT TTG TGT TAT TAG-3' (-) SEQ ID NO: 2; ending at base 345. The 3' half of *ospC* was amplified using the primer, 5'-TTG TTA 20 GCA GGA GCT TAT GCA ATA TC-3' (+), SEQ ID NO: 3, beginning at base 289, and SEQ ID NO: 4 as the reverse primer. The external primers amplified a 597 bp fragment. Amplification of the 5' half produced a 340 bp fragment while amplification of the 3' half produced a 314 bp fragment. All the base numbers and amplified fragment sizes are based on *ospC* sequence of strain B31 (GenBank accession number U01894), with start codon as base 1.

Amplification was conducted in 50µl of a solution containing Perkin-Elmer 25 Cetus 10x PCR buffer (100 mM Tris-HCl (pH 8.3), 500 mM KCl), 2.5 mM MgCl₂, deoxynucleoside triphosphates at 0.2 mM per nucleotide, 2.5 U of Taq polymerase (Perkin-Elmer/Cetus) and 0.5 µM of each primer. The amplification reaction was

carried out for forty cycles in a DNA thermal-cycler (PTC-100; MJ Research, Inc., Watertown, MA) with an amplification profile of: denaturation at 95°C for 40 seconds, annealing at 54°C for 35 seconds, and extension at 72°C for 1 min, after an initial denaturation step at 96°C for 2 min. Negative controls were included in each experiment
5 to control for contamination.

Cold SSCP-analysis.

SSCP analysis was chosen to characterize genetic variation of the isolated *ospC* gene fragments based on its exquisitely high detection rate of DNA polymorphisms and point mutations at a variety of positions in DNA fragments (Orita, M. *et al.*, *Proc. Natl. Acad. Sci.* 86:2766-2770, (1989)). Single point mutations have been detected in fragments up to 800bp long (Michaud, J. *et al.*, *Genomics*. 13:389-394, (1992)). However, there is evidence that the ability of SSCP analysis to detect mutations begins to decline significantly as PCR fragments approach 400bp in size (Hayashi, K., *PCR Methods & Applications* 1:34-38, (1991)). Therefore, in order to achieve high efficiency
10 of detection of nucleotide polymorphism, the length of the PCR products used herein
15 was 340bp from the 5' half and 314bp from the 3' half of *ospC*.

Amplified *ospC* gene fragments from all one hundred and forty strains were analyzed for genetic variations by the cold SSCP protocol described by Hongyo *et al.* (Hongyo, T. *et al.*, *Nucleic Acids Res.* 21:3637-3642, (1993)). Briefly, 5 to 15 µl of the
20 PCR product was added to a mixture containing 4 µl 5x TBE Ficoll sample Buffer (NOVEX, San Diego, CA) and 0.4 µl 1 µM methylmercury hydroxide (Alfa Aesaer, Ward Hill, MA). The amount of the PCR product used for the SSCP analysis was estimated after visualizing the PCR product on an agarose gel with ethidium bromide. The sample mixture was heated to 95°C for 4 min, then chilled on ice prior to loading
25 the entire 20 µl into the gel sample well. The sharpest bands were observed when the sample was applied to a pre-cast 20% TBE gel (NOVEX) electrophoresis system (ThermoFlow ETC Unit, NOVEX) with 1.25x TBE running buffer. Electrophoresis of

SSCP products was conducted at a constant temperature of 8°C for 17 h at 240 volts in order to reveal discernable mobility shifts. Gels were stained with 0.5 µl/ml ethidium bromide in 1x TBE buffer for 25 min and destained in distilled water for 30 min.

- Stained bands were viewed using a 340nm UV staining box. Samples that showed more than two SSCP bands were reamplified to determine whether the bands found were real alleles or the product of PCR artifacts. Side-by-side SSCP analysis was performed in order to detect even slight shifts in electrophoretic mobility.

DNA sequencing

- The *ospC* gene or representatives of each mobility class were reamplified.
- Double-stranded PCR fragments were purified by agarose gel electrophoresis and subjected to automated DNA sequencing using fluorescent dideoxy terminator chemistry and the forward and reverse primers originally used for PCR amplification.

Statistical analysis

- Chi square analysis of contingency tables was performed. This analysis tests for significant difference in frequency distributions. The tables were 2xN where N is the number of major *ospC* groups distinguished. The average expected number in each element of the table needs to be about six or greater for an unbiased test (Zar, J.H., *Biostatistical Analysis*, 3rd ed, p. 206, (1996)). This means that the number of observations should be greater than 6 times 2N. When the expected average number was less than six, the major *ospC* groups with the lowest number in the sample were combined until the number of observations were about equal to or greater than 12N.

RESULTS

ospC mobility classes in human *B. burgdorferi* isolates.

- One hundred and thirty-two isolates of *B. burgdorferi* sensu stricto from patient samples of skin, blood, and CSF (Table II) were propagated *in vitro* and used as a source

of DNA for analysis. The *ospC* genotype of each strain was determined by cold SSCP analysis of the 5' end (340bp) of the gene and was confirmed by SSCP analysis of the 3' end (314bp) of *ospC*. In all *B. burgdorferi* isolates, the genetic variation at the 5' end of the gene corresponded to the variation at the 3' end. At least two representatives of each 5 SSCP mobility class were subsequently sequenced. The sequences of the same mobility classes were identical in all samples and each mobility class had a unique sequence. Therefore, the sensitivity and specificity of SSCP analysis was 100%. Each SSCP mobility class was designated as an allele. Wang *et al.* recently described 13 *ospC* alleles (Wang, I-N. *et al.*, *Genetics* 151:15-30). An additional five *ospC* (OC) mobility 10 classes, OC14-18 are described herein. OC14 has the same *ospC* sequence as the *ospC* in strain 2591.

TABLE II. Alignment of major *ospC* groups with *ospC* alleles identified by SSCP analysis

Major <i>ospC</i>	<i>ospC</i> allele	GenBank		Dis-	
Group	(SSCP)	number ¹	Ticks	seminated ²	
5	A	1	AF029860	17	23
	B	2	AF029861	17	19
	C	3	AF029862	11	3
	D	4	AF029863	10	1
	E	5, 7	AF029864	6	1
10	F	6	AF029865	9	0
	G	8	AF029867	5	7
	H	9	AF029868	7	6
	I	10	AF029869	1	9
	J	11, 18	AF029870	3	7
15	K	12, 13	AF029871	6	32
	L	-	L42899	2	0
	M	14	U01892	1	3
	N	15	L42899	1	3
	O	-	X84778	0	1
20	P	-	U91796	1	0
	Q	-	U91790	1	0
	R	-	U91791	2	0
	S	-	U91793	1	0
	T	16	AF065143	0	1
25	U	17	AF065144	0	2

¹ A single GenBank sequence of each type is given as an example.

² The number of each major *ospC* group observed in blood, synovial fluid or cerebrospinal fluid. This includes both SSCP data and data from the literature, including GenBank.

5 **B. burgdorferi* sensu stricto Groups P through S are only found in Europe. Groups R and S are excluded from the analysis because nearly identical *ospC* alleles are found in *B. afzelii* and *B. garinii*, showing these groups were recently created by cross-species transfer.

10 10 Multiple infections

Of the one hundred and thirty-two primary isolates from patients with Lyme disease in this study, most contained only a single strain. Seven skin isolates and one CSF isolate contained two different strains as determined by SSCP analysis, thus giving a total of one hundred and forty different strains. The *ospC* allele pairs found in 15 multiply infected erythema migrans biopsy specimens were (OC1, OC12), (OC1, OC14), 2x(OC2, OC3), 2x(OC2, OC12), and (OC8, OC18). CSF isolate NY940657 contained *ospC* alleles OC1 and OC12. For CSF isolate 297, which was isolated in Connecticut, there were two *ospC* sequences published in GenBank: L42893, which is analogous to OC10 and U08284, which is analogous to OC12. The pair-wise difference 20 of *ospC* sequences of both strains is 16.4%, suggesting CNS infection with two different strains in this isolate. Overall, 5.5% of all isolates described herein contained two strains. Because as many as 50% of ticks isolated in the wild are infected with multiple strains, exposure to multiple strains in a single tick bite is common, raising the possibility that different strains are differentially pathogenic.

25 To these one hundred forty strains for which the *ospC* allele was determined herein, twenty-two strains of known *ospC* sequence from GenBank were added to give a total of one hundred sixty-two. Fifty-one of these strains were obtained either from

eastern Long Island; seventy-seven were obtained from Westchester County, New York, and the remainder from other endemic areas in the United States (twenty-two strains) and Europe (twelve strains). The isolates were divided into those from the site of the primary infection, the erythema migrans skin lesion (one hundred eighteen isolates), and 5 those from secondary sites, where the infection had disseminated (forty-four isolates). This later group included, for example, twenty from cerebro-spinal fluid (CSF), twenty-three from blood, and one from synovial fluid.

Major *ospC* groups in human *B. burgdorferi* isolates

Surprisingly, as described herein, the differences between *ospC* sequences 10 among and between the families of *B. burgdorferi* sensu stricto fell into two groups. Pairs of *ospC* genes within the same family differed in nucleic acid sequence by less than two percent while pairs of *ospC* genes from separate families in nucleic acid sequence differed by more than eight percent. Wang *et al.*, defined nineteen major *ospC* groups, designated A to S (Wang, I-N. *et al.*, *Genetics* 151:15-30 (1999)). As described 15 herein, two additional *ospC* groups are provided, designated T and U. OC16 represents major group T and OC17 represents major group U (Table I). The lowest pair-wise differences of group T and U to any other major *ospC* group are 16.1% and 20.5% respectively.

B. burgdorferi clones are differentially pathogenic

20 As described herein, clones representing different *ospC* groups of *Borrelia burgdorferi* are differentially pathogenic. This is demonstrated by the differing frequencies of the various major *ospC* groups in ticks, in the initial infection in the skin, and in disseminated infections.

The strains in GenBank and the literature for which the *ospC* sequences have 25 been determined were widely sampled from the entire geographic range of the species and were chosen irrespective of whether they were from ticks or humans. These strains

gave a small but random sample of the frequencies of the major *ospC* groups in ticks and humans. As demonstrated herein, the frequency of the major *ospC* groups from human isolates was found to be significantly different from the frequency found in ticks on Long Island. Table III shows that the frequency distribution of strains from skin 5 from eastern Long Island differ significantly from tick strains collected in the same area.

TABLE III

	Major <i>ospC</i> groups	A	B	C	D	F	G	H	I	K	Comb. ^a
	Isolates From										
	Erythema migrans	13	6	2	0	0	1	0	4	16	4
10	lesions (N=46)										
	Ixodes scapularis	12	12	11	9	6	5	7	1	5	6
	ticks (N=74)										

$$\chi^2 = 36.3 \text{ with 9 degrees of freedom}$$

$$p < 0.001$$

^a Combined major groups are defined by individual frequencies of 0.025 or less and include groups E, J, N, O.

15 The analysis provided herein of all *ospC* groups presented in this study showed that most groups are found in both ticks and in humans (Table II). However, major groups A, B, I and K predominated in humans, with A and K groups found most frequently. (Figure 1).

The pattern of pathogenicity of the various clones as demonstrated by frequency 20 in the primary site of infection, the skin, compared to the frequency in secondary sites revealed that only four major groups (A, B, I and K) were found in both the skin and secondary sites (compare Tables III and IV). All other major groups were found only in the skin. When all groups with three or fewer isolates are combined to give the

combined group of Table IV, a 2 by 8 contingency test comparing the frequency distribution of skin versus secondary sites gives a significance of $p<0.005$. When no groups are combined, a 2 by 15 contingency test is still significant ($\chi^2 = 24.07$ with 14 degrees of freedom, $p<0.05$). The distribution of strains from primary and secondary
5 sites indicated that only a certain of the major groups, A, B, I, and K cause disseminated disease. As described herein, these are referred to as invasive clones whereas other clones are referred to as non-invasive clones.

TABLE IV

	Major <i>ospC</i> groups	A	B	G	H	I	J	K	Comb. ^a
10	Isolates From								
	Erythema migrans	23	19	7	6	9	7	32	16
	lesions (N=118)								
	Disseminated Infections	21	4	0	0	3	0	16	0
	(N=44)								

$\chi^2 = 23.6$ with 7 degrees of freedom
 $p<0.005$

15 ^a Combined major groups are defined by individual frequencies of 0.025 or less and include groups C, D, E, M, N, O, T and U.

As described herein, the different clones of *B. burgdorferi* sensu stricto, as defined by *ospC* groups, are differentially pathogenic. Some groups very rarely, if ever, cause human disease, e.g. *ospC* groups D, E, F, and L. Some groups cause a local
20 infection at the tick bite site, but not systemic disease, e.g. *ospC* groups G, H, J, and T. Finally, there are some groups which are responsible for systemic disease; these are

ospC groups A, B, I, and K. Our findings indicate that all systemic *B. burgdorferi* sensu stricto infections in humans are caused by strains in these four *ospC* groups.

Figure 1 shows the frequency distribution of major *ospC* groups among *B. burgdorferi* isolates from Eastern Long Island *Ixodes scapularis* ticks, n=72, (A); erythema migrans lesions, n=118, (B); and secondary sites of infection, n=44, (C). The percentage of group A plus K increased from 23% in the tick isolates, to 47% in the skin isolates, and to 84% in the secondary sites. The length of the bars in Figure 1 reflect this increase, by holding the length of the combined A and K groups constant. In the skin, groups C, D, E, M, N, O, T and U have been combined since their individual frequencies are 0.025 or less. This combination of groups when combined make up 12.7% of the total number of strains.

A similar analysis was conducted for *Borrelia afzelii*. The analysis included *OspC* alleles from 21 strains from GenBank and 12 strains sequenced for this study. These sequences fell into 20 major groups where the definition of a group is less than 1% sequence diversity within a group and at least 7.7% sequence difference between groups. There were two exceptions to this rule which were caused by a deletion in one *ospC* gene and a cross-species transfer of a small section of DNA in another *ospC* gene. When these anomalous sections were removed, all *ospC* alleles fell into 20 groups. Only two groups contained strains from chronic infections - groups A and B. By analogy and the *B. burgdorferi* study, it appears that only two groups are pathogenic in *B. afzelii*.

EXAMPLE 2: Protein Expression and Immunoblot

Protein Expression

The *Escherichia coli* (strain BL21 (pLysS) or strain B834 (DE3)) were transformed with the plasmid encoding the recombinant chimeric *Borrelia* proteins (RCBPs), and grown in 10 ml LB media (5 g/l NaCl, 10 g/l tryptone, 5 g/l yeast extract, 25 mg/l chloramphenicol and 50 mg/l ampicillin) at 37°C, with shaking. When the

optical density at 600λ reached 0.3-0.4 units, recombinant protein expression was induced by adding IPTG (isopropyl B-D-thiogalactopyranoside) to a final concentration of 0.5 mM and the cells were grown for an additional three hours. The cultures were harvested by centrifugation at 3800xg for five minutes. The cells were resuspended in
5 20 mM NaPO₄, pH7.7 and stored at -20°C overnight. Once thawed, the crude extracts were incubated with DNase (2 µg/ml) in the presence of 2.5 mM of MgCl₂ at room temperature for thirty minutes, spun at 14000 rpm (Eppendorf 5417C) for five minutes and 5 µl of the protein sample was run on a SDS-PAGE which was either stained in Commassie Blue or used for Immunoblot. Protein samples were solubilized, usually
10 with a sodium dodecyl sulphate (SDS) containing buffer and in selected cases with reducing agents such as dithiothreitol (DTT) or 2-mercaptoethanol (2-ME). Following solubilization, the material was separated by SDS-PAGE. The proteins were then eletrophoretically transferred to a polyvinylidene difluoride membrane (PVDF, Immobilon-P®, Millipore). The transfer of proteins was monitored by a reversible
15 staining procedure, Ponceau S. The stained membrane was made and the membrane destained by soaking in water for 10 minutes. All non-specific binding sites in the proteins and on the membrane were blocked by immersing the membrane in a solution containing a protein or detergent blocking agent (5 % milk in tris-buffered saline (TBS) Tween-20® 0.1%). The membranes were then incubated with primary antibody (either
20 a monoclonal antibody or Erythema Migrans Lyme disease human serum). The membrane was washed and the antibody-antigen complexes were identified using alkaline phosphatase (AP) enzymes coupled to secondary antibody, either anti-immunoglobulin G (anti-mouse IgG) to detect the monoclonal antibody or anti-human IgA+IgG+IgM to detect the serum antibodies. A chromogenic substrate for alkaline
25 phosphatase was then used to visualize the activity.

EXAMPLE 3: SEROLOGIC CHARACTERIZATION - ELISA (Enzyme-Linked
Immunosorbent Assay)

Immobilization of RCBPs onto ELISA Plates, Determining Optimal RCBP
Binding:

5 A solution of purified RCBPs in sodium phosphate buffer, pH 9.0 was used to
coat commercial microwell plates (MaxiSorp®, Nunc). Recombinant OspC *Borrelia*
proteins are described in Table V. The coating procedure was as follows: 100 µl of a
solution containing the appropriate concentration of each RCBP was added to each well
and the microwell plate was incubated for either one hour at room temperature or at 4°C
10 overnight. The antigen solution was removed from the wells, the plate washed three
times with phosphate buffered saline (PBS) pH 9.0, and 200 µl of blocking solution
added (2% BSA fraction V (Sigma) in PBS). Following a thirty minute incubation at
37°C, the plates were washed three times with PBS, wrapped in plastic and stored at
4°C until used. The binding of the individual RCBPs was measured using monoclonal
15 antibodies specific for either OspA or OspC followed (after washing) by an alkaline
phosphatase-conjugated goat anti-mouse secondary antibody. The upper limit of
protein binding was found to be beyond the working range of the monoclonal antibody
used to measure it, and the standard blocking protocol was found to successfully
saturate this high protein binding capacity, leaving low background readings in the
20 control wells. The results of these experiments indicated that a protein concentration of
0.5 µg/ml in the coating buffer was optimal for each of the RCBP tested. It was not
found to be necessary that the chimeric proteins be immobilized in a specific molar ratio
to one another; only that enough of each protein be bound so that epitopes in that
chimeric protein do not become limiting in subsequent ELISA assays using patient
25 serum. For practical purposes, it was found that these conditions were met when the
monoclonal-capture assay reached an absorbance of about 1.5 units or greater for each
mouse monoclonal antibody, with a specific epitope represented in one of the chimeric
proteins on the well surface. If necessary, however, the concentrations of individual

proteins in the mixture can be adjusted to achieve the desired levels of immobilized protein using routine optimization. Although the amount of each RCBP bound to the surface of the well and the amount of any one epitope exposed to the solution varies somewhat from protein to protein, the amount of bound epitope was not found to be
5 limiting within the useful range of the ELISA.

ELISA Tests:

The standard procedure for the ELISA tests was as follows: human serum samples were diluted 1:100 in specimen diluent (10% fetal bovine serum in PBS pH 9.0) and 100 µl of each sample added to ELISA plate microwells that had been coated
10 with antigen as described above. Following incubation for 1 hour at 37°C, the samples were removed and the plates washed three times in TBS-Tween™ (0.5 M Tris pH 7.2; 1.5 M NaCl; 0.5% Tween™). Goat anti-human antisera conjugated to alkaline phosphatase specific for either IgM (Fc) or IgG (Fab), (Jackson Immuno Research Laboratories) was diluted 1:1000 in PBS, pH 7.4 and 100 µl of the solution added to
15 each well. Following incubation for thirty minutes at 37°C, the plates were washed three times with TBS-Tween™ and 100 µl of substrate solution (5 mg of p-nitrophenylphosphate tablets dissolved in 1X diethanolamine substrate buffer to yield a 2 mg/ml solution - Kirkegaard Perry Laboratory) was added to each well. The plates were incubated for thirty minutes at 37°C and 100 µl of stop solution (5 % EDTA) was
20 added to each well. The absorbance at 410 nm was read on a microplate reader (Dynatech). A sample was considered positive if it produced an average absorbance greater than the mean of the negative controls plus three standard deviations. Cross-reactivity was measured against serum from patients with syphilis, systemic lupus erythematosus, rheumatoid arthritis as well as endemic field workers and non-endemic
25 field worker.

Using the above-described ELISA test, serum from various patients was tested. Patients with Erythema Migrans Acute (EMA) had early, localized infections, typified

by the presence of well-defined erythema migrans (EM) in patients from an endemic area. Patients with Early Disseminated (EA), are Acute Disseminated (AcD) infections were typified by EM and one of the following: additional EM lesions, AV block, neurological abnormalities (e.g., seventh nerve palsy), or meningitis. Patients with
5 Acute Convalescent (AcC) were obtained from the same patients as EA and AcD, 2-4 weeks later. Serum was also tested from the CDC from patients with well documented Syphilis (S), serum was also obtained from SUNY at Stony Brook, Division of Rheumatology from patients with well documented systemic Lupus Erythematosus (SLE) or patients with well documented Rheumatoid Arthritis (RA). Endemic field
10 worker sera (End), were obtained from outdoor workers from Long Island, which is endemic for Lyme disease. Non-endemic sera (Nedn) were obtained from outdoor workers from Arizona, which is not endemic for Lyme disease. In addition, serum was tested from endemic field workers (End) and non-endemic field workers (NEnd).
Polypeptides of the present invention were used to test these various sera as summarized
15 in Figure 8.

Table V

Polypeptide	SEQ ID NO.* (DNA)	SEQ ID NO: (POLYPEPTIDE)
C1 unlipidated	5	6
C2 unlipidated	7	8
⁵ C1	9	10
C2	11	12
C5	13	14
C7	15	16
¹⁰ C10	17	18
C11	19	20
C12	21	22
C1C10 ²	23	24
C1C12	25	26
¹⁵ B31C10 ³	27	28
B31C12	29	30
C2C7	31	32
C2C10	33	34
C2C12	35	36
²⁰ C5C7	37	38
C5C10	39	40
C5C12	41	42

¹ C1-C12 are OspC genes/proteins with lipidation signal.

² C2C10 and other compound C names refer to chimeric OspC proteins wherein the N-terminal portion of the chimera is derived from a first *ospC* allele and the C-

terminal portion of the chimeric molecule is derived from second *ospC* allele, as described herein. The polypeptides were not lipidated.

EXAMPLE 4: MICE IMMUNIZATION WITH OSPC CHIMERIC PROTEINS AS
5 IMMUNOGEN

- Female BALB/c mice, four-five weeks old, were immunized with 5 µg of OspC chimeric proteins in 100 µl of aluminum hydroxide adjuvant by SC (subcutaneous) injection. Five mice were used for each group. For the negative control, five female BALB/c mice were immunized with 100 µl of aluminum hydroxide adjuvant only.
- 10 Two weeks after immunization, the mice received a boost with the same antigen and two weeks after that an equal boost was administered. One week after each boost, blood was drawn from each mouse (including negative controls) and the serum was tested, using the ELISA method described above, for the presence of the respective anti-OspC chimeric protein antibodies.
- 15 Mice were immunized with chimeric proteins as follows in Table VI.

TABLE VI

	Immunogen	SEQIDNO.: (polypeptide)	OspC Family
	LipCB31 ¹	44 (DNA 43)	A
5	LipC12 ²	22 (DNA 21)	K
	UnlipC2 ³	8	B
	UnlipC2C7 ⁴	32	B/E
	UnlipC2C10	34	B/I
	UnlipC2C12	36	B/K
10	UnlipC5C10	40	E/I
	UnlipC5C12	42	E/K

¹ "Lip" means lipidated N-terminus, Lip CB31 is OspC protein from *B. burgdorferi* strain B31.

² The number immediately after "C" refers to the particular allele of OspC as described herein.

¹⁵ ³ "Unlip" means the unlipidated form of the N-terminus.

Several types of single OspCs from *B. burgdorferi sensu stricto*, OspCB31, OspC2, OspC5, OspC7, OspC10, OspC12 and a single OspC from *B. afzelii*, Ctro, were used as the antigens in an ELISA to test the serum collected from the immunized mice. As shown in Figures 2 and 3, unlipC2C10 and unlipC2C12 elicited an immune response in the form of antibodies, (a humoral response) against a broad range of *ospC* families, after the first and second bleeds, respectively. The serum from unlipC2C10, unlipC2C12, LipCB31 and LipC12 immunized mice was then used to test against single OspC polypeptides from several strains of the three major *Borrelia* gene species *Borrelia burgdorferi*, *Borrelia afzelii* and *Borrelia garinii*.

As shown in Figure 4, 13 different strains of *B. burgdorferi sensu stricto* (*B.b.s.s.*) were tested for reactivity with the above described sera. Sera from mice immunized with both LipCB31 and LipC12, which were the gold standard of this

experiment, detected 12/13 of the *B.b.s.s.* strains tested. Sera from mice immunized with unlipidated C2C12 detected 8/13 of the strains tested. Use of unlipidated forms of these proteins as vaccine immunogens or diagnostic antigens is desirable because the product yield by the expression vector is much greater and the proteins are much easier 5 to purify. These two reasons alone made the production of these proteins less expensive.

As shown in Figure 5, chimeric proteins unlipC2C10 and unlipC2C12 of the present invention elicited an immune response that detected 5/6, and 6/6 of the strains tested, as compared to the gold standard lipidated proteins LipC12 and LipCB31, which 10 detected 5/6 and 3/6 of the strains, respectively. When compared to the parental unlipidated OspC2 (rOspC2), the chimeric proteins unlipC2C10 and unlipC2C12 elicited an immune response and detected more strains than the gold standard ((0/6) versus (5/6) and (6/6) respectively). This result was unforeseen and unexpected.

In another experiment, as shown in Figures 6 and 7, chimeric proteins of the 15 present invention elicited a significant immune response across all the 18 different strains of *B. afzelii* (Fig. 6) and all the 21 different strains of *B. garinii* (Fig. 7). For example, the chimeras unlipC2C10 and unlipC2C12 detected 12 and 18 of the 18 strains of *B. afzelii*, respectively, as compared to 0/18 detected by the parental unlipidated C2. The same chimeras detected 14 and 20 of the 21 strains of *B. garinii*, 20 respectively, as compared to 0/21 detected by the parental unlipidated C2. Furthermore, the gold standards LipCB31 and LipC12 detected 2 and 17 of the 18 strains of *B. afzelii*, respectively, and 2 and 15 of the 21 strains of *B. garinii*. These results indicate that, unlike the LipOspCB31, LipOspC12 and unlipOspC2, the unlipidated C2C10 and unlipidated C2C12 used as immunogens elicited a significant 25 immune response across all the different strains of *B. burgdorferi*, *B. afzelii* and *B. garinii* tested.

Additional chimeras were constructed and are listed in Table VII.

TABLE VII
OspC Polypeptides and Chimeric Polypeptides of the Present Invention

	POLYPEPTIDE	SEQ ID NO.:(DNA)	(POLYPEPTIDES)
	¹ unlip OspC kkp(55-621*)	45	46
5	unlip OspC PKO	47	48
	unlip OspC TRO	49	50
	² unlip OspC-55B31/ 58PKO/56TRO	51	52
	unlip OspC1-TRO	53	54
10	unlip OspC-TRO	55	56
	³ Blip OspC1C10	59	60
	BlipOspC12	61	62
	Blip OspC1-TR0	77	78
	Blip OspC2C7	67	78
15	Blip OspC2C10	63	64
	Blip OspC2C12	65	66
	Blip OspC2-TRO	69	70
	Blip OspC5C7	75	76
	Blip OspC5C10	71	72
20	Blip OspC5C12	73	74
	Blip OspCB31C10	79	80
	Blip OspCB31C12	81	82
	Blip OspCPkoTro	83	84
25	Blip OspC- 55B31/58Pko/56Tro	85	86

¹Ulip means the polypeptide is unlipidated.

²An OspC chimera comprised of 3 OspC polypeptides.

³Blip means the polypeptide is lipidated due to the gene having the OspB lipidation signal on the 5' terminus.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims.

CLAIMS

What is claimed is:

1. A composition comprising OspC polypeptides from Lyme Disease causing *Borrelia* wherein either:
 - 5 a) said composition comprises one or more OspC polypeptides or immunogenic fragments thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A, B, I and K, excepting the combination consisting of two OspC proteins wherein one OspC protein is from family A and the second OspC protein is from family I, or;
 - 10 b) said composition comprises at least one OspC polypeptide or immunogenic fragment thereof from each of *Borrelia afzelii* OspC families A and B.
2. The composition of Claim 1 comprising one or more OspC polypeptides or fragments thereof from each of *Borrelia burgdorferi* families of the group of subpart a).
- 15 3. The composition of Claim 1, wherein said OspC polypeptide or fragment thereof comprises the OspC protein variable region.
4. The composition of Claim 3, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 26 to about 20 nucleotide 621 of an *ospC* gene.

5. The composition of Claim 3, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 53 to about nucleotide 570 of an *ospC* gene.
6. The composition of Claim 1, wherein at least two of said OspC polypeptides or 5 immunogenic fragments thereof are fused together in a single protein, encoded by a single nucleic acid, wherein polypeptides in said fusion protein are not found in the same configuration in a naturally occurring OspC protein.
7. The composition of Claim 1, wherein the *ospC* genes encoding the OspC polypeptides within a given OspC family are at least 98% identical at the 10 nucleic acid level.
8. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, Pka, Txgw and strains containing *ospC* allele OC1.
9. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family B 15 comprises strains 35B808, 61 BV3, BUR, DK7, PB3, Z57 and strains containing *ospC* genes OC2 and OC3.
10. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family I comprises strains 297, HB19 and strains containing *ospC* gene OC10, wherein strain 297 is characterized by *ospC* of GenBank accession number L42893.
- 20 11. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family K comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC*

gene OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank accession number U08284.

12. The composition of Claim 1, wherein *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, PKO, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB.
- 5 13. The composition of Claim 1, wherein *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 134M.
14. A method of immunizing an animal against Lyme disease, comprising administering a composition comprising at least two OspC polypeptides from Lyme Disease causing *Borrelia* wherein either:
 - 10 a) said composition comprises one or more OspC polypeptides or fragments thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A, B, I and K, excepting the combination consisting of two OspC proteins wherein one OspC protein is from OspC family A and the second OspC protein is from OspC family I, or;
 - b) said composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B.
15. The method of Claim 14, wherein the composition comprises one or more OspC polypeptides or fragments thereof from each of *Borrelia burgdorferi* families of the group of subpart a).
- 20 16. The method of Claim 14, wherein said OspC polypeptide or fragment thereof comprises the OspC protein variable region.

17. The method of Claim 14, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 26 to about nucleotide 621 of an *ospC* gene.
18. The method of Claim 14, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 53 to about nucleotide 570 of an *ospC* gene.
19. The method of Claim 14, wherein at least two of said OspC polypeptides or immunogenic fragments thereof are fused together in a single protein, encoded by a single nucleic acid, wherein polypeptides in said fusion protein are not found in the same configuration in a naturally occurring OspC protein.
20. The method of Claim 14, wherein the *ospC* gene encoded the OspC polypeptides within a given OspC family are at least 98% identical at the nucleic acid level.
21. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, Pka, Txgw and strains containing *ospC* allele OC1.
22. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family B comprises strains 35B808, 61 BV3, BUR, DK7, PB3, Z57 and strains containing *ospC* genes OC2 and OC3.

23. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family I comprises strains 297, HB19 and strains containing *ospC* gene OC10, wherein strain 297 is characterized by *ospC* of GenBank accession number L42893.
24. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family K comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC* gene OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank accession number U08284.
25. The method of Claim 14, wherein *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, PKO, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB.
- 10 26. The method of Claim 14, wherein *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 134M.
27. A method of detecting an immune response to Lyme Disease causing *Borrelia* in a host sample, comprising;
- 15 a) contacting the host sample with a composition comprising OspC polypeptides from Lyme disease causing strains of *Borrelia*, such that anti-OspC antibodies, if present in said sample bind to said OspC polypeptides; wherein
- i) said composition comprises one or more OspC polypeptides or fragments thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A, B, I and K, excepting the combination consisting of two OspC proteins wherein one OspC protein is from family A and the second OspC protein is from family I, or;
- 20

- ii) said composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B; and
- 5 b) detecting antibodies that have bound said OspC peptides; thereby detecting an immune response to Lyme disease causing *Borrelia*.
28. The method of Claim 27, wherein said OspC polypeptide or fragment thereof comprises the OspC protein variable region.
29. The composition of Claim 27, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 26 to about 10 nucleotide 621 of an *ospC* gene.
30. The composition of Claim 27, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 53 to about nucleotide 570 of an *ospC* gene.
31. The composition of Claim 27, wherein at least two of said OspC polypeptides or immunogenic fragments thereof are fused together in a single protein, encoded by a single nucleic acid, wherein polypeptides in said fusion protein are not found in the same configuration in a naturally occurring OspC protein.
- 15 32. The method of Claim 27, wherein the *ospC* genes encoding the OspC polypeptides within a given OspC family are at least 98% identical at the 20 nucleic acid level.

33. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, Pka, Txgw and strains containing *ospC* allele OC1.
34. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family B comprises strains 35B808, 61 BV3, BUR, DK7, PB3, Z57 and strains containing *ospC* genes OC2 and OC3.
- 5 35. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family I comprises strains 297, HB19 and strains containing *ospC* gene OC10, wherein strain 297 is characterized by *ospC* of GenBank accession number L42893.
- 10 36. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family K comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC* gene OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank accession number U08284.
- 15 37. The method of Claim 32, wherein *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, PKO, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB.
38. The method of Claim 32, wherein *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 134M.
- 20 39. A chimeric protein comprising OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said chimeric protein comprises:

- a) a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 26 to about nucleotide 621 of an *ospC* gene from a first OspC family and
 - b) a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 28 to about nucleotide 570 of an *ospC* gene from a second OspC family.
- 5
40. The chimeric protein of Claim 39, wherein said OspC families are selected from the group consisting of: *Borrelia burgdorferi* OspC families A, B, I and K, and *Borrelia afzelii* OspC families A and B.
- 10 41. A chimeric protein comprising OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said chimeric protein comprises:
- a) a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 53 to about nucleotide 570 of an *ospC* gene from a first OspC family and
 - b) a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 28 to about nucleotide 570 of an *ospC* gene from a second OspC family.
- 15
42. The chimeric protein of Claim 41, wherein said protein is unlipidated.
- 20 43. A chimeric OspC protein selected from the group consisting of: SEQ Id Nos: 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84 and 86.

44. An isolated nucleic acid encoding a chimeric protein wherein said protein comprises OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said chimeric protein comprises:
- 5 a) a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 26 to about nucleotide 621 of an *ospC* gene from a first OspC family and
- b) a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 28 to about nucleotide 570 of an *ospC* gene from a second OspC family.
- 10
45. The nucleic acid of Claim 44, wherein said OspC families are selected from the group consisting of: *Borrelia burgdorferi* OspC families A, B, I and K, and *Borrelia afzelii* OspC families A and B.
46. The nucleid acid of Claim 44, wherein said protein is unlipidated.
- 15 47. A isolated nucleic acid comprising OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said isolated nucleic acid comprises:
- a) a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 53 to about nucleotide 570 of an *ospC* gene from a first OspC family and
- 20 b) a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 28 to about nucleotide 570 of an *ospC* gene from a second OspC family.

48. An isolated nucleic acid selected from the group consisting of : SEQ ID Nos:
23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 51, 53, 55, 56, 59, 61, 63, 65, 67, 69, 71,
73, 75, 77, 79, 81, 83 and 85.

GROUPS OF *BORRELIA BURGDORFERI* AND *BORRELIA AFZELII*
THAT CAUSE LYME DISEASE IN HUMANS

ABSTRACT OF THE DISCLOSURE

- The present invention is drawn to an immunogenic composition comprising
- 5 OspC polypeptides from Lyme Disease causing *Borrelia*. In one embodiment, the immunogenic composition of the present invention comprises at least one OspC polypeptide or immunogenic fragment thereof from each of *Borrelia burgdorferi* OspC families A, B, I and K. In another embodiment, the immunogenic composition of the present invention comprises at least one OspC polypeptide or immunogenic fragment
- 10 thereof from each of *Borrelia afzelii* OspC families A and B.

PCT/US2002/01002-001

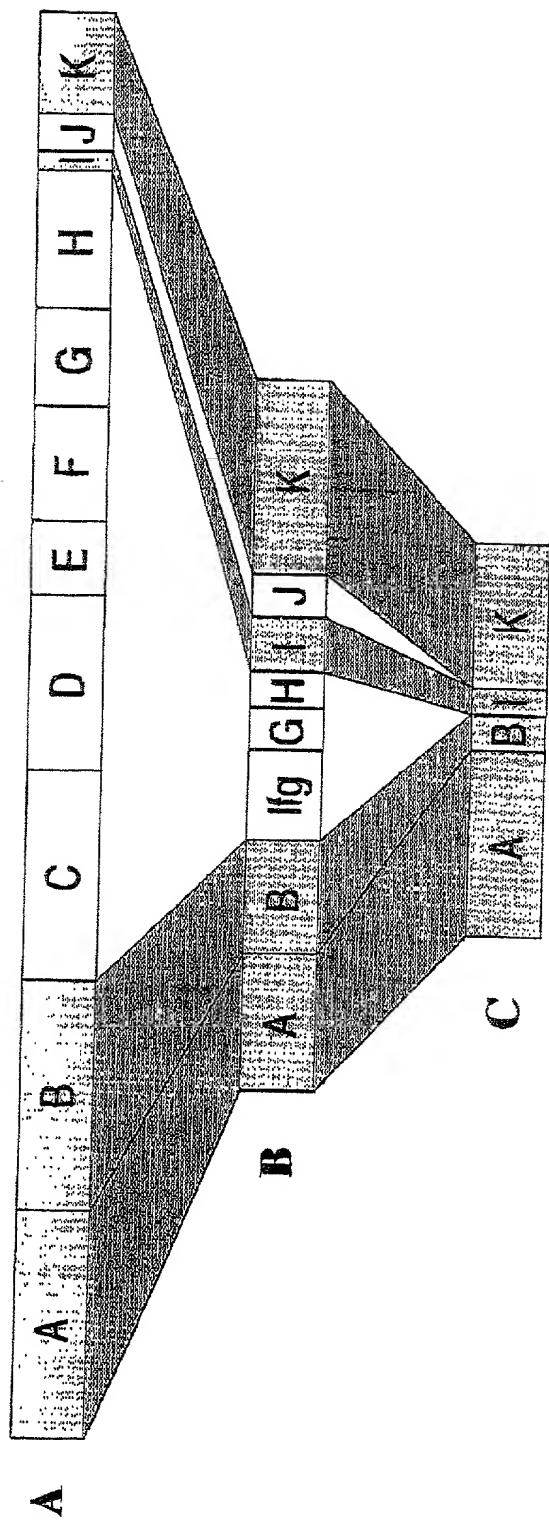


Fig. 1

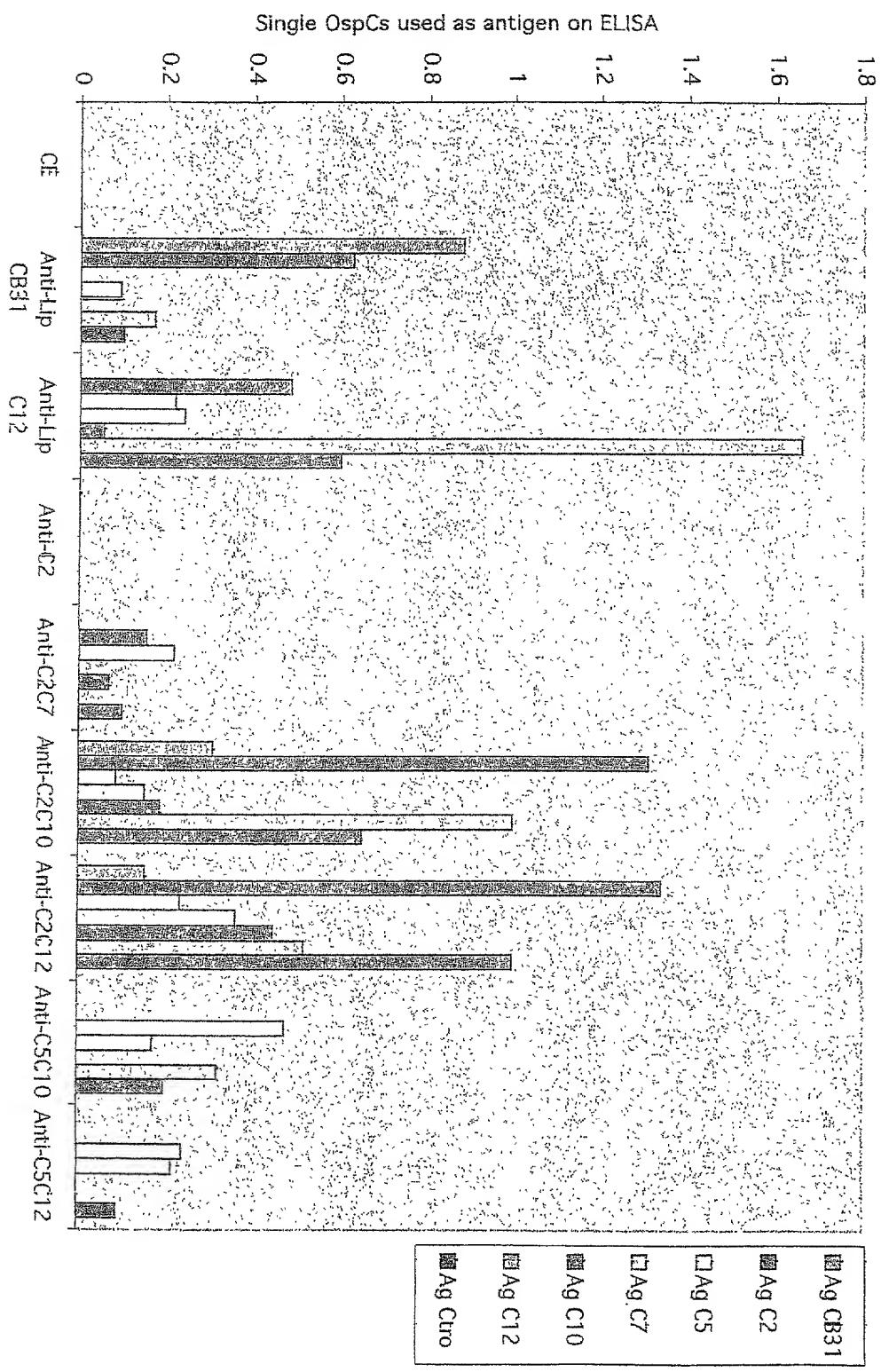


Fig. 2

Serum from OspC-RCBP vaccinated mice (1st Bleed)

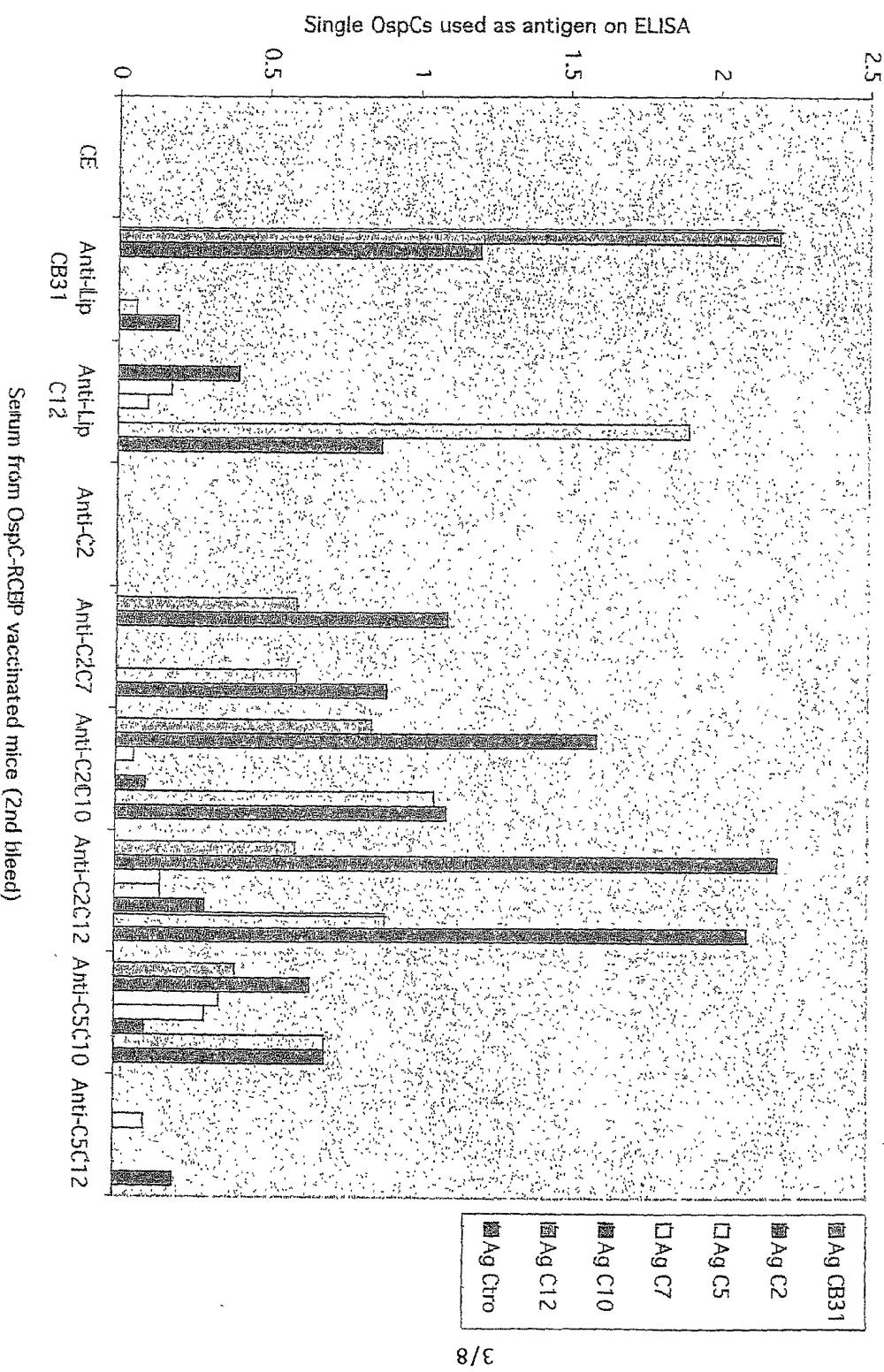


Fig. 3

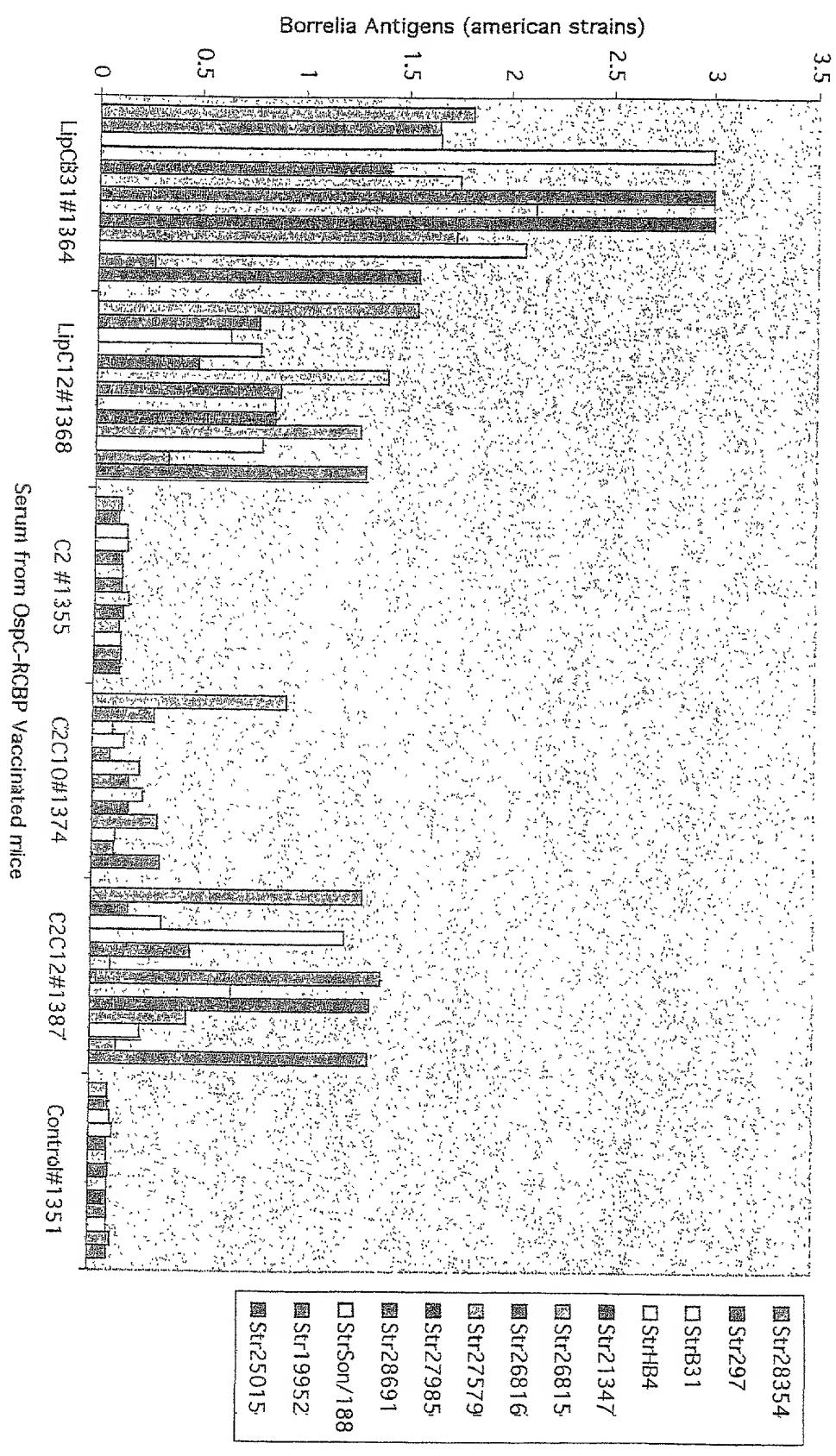


Fig. 4

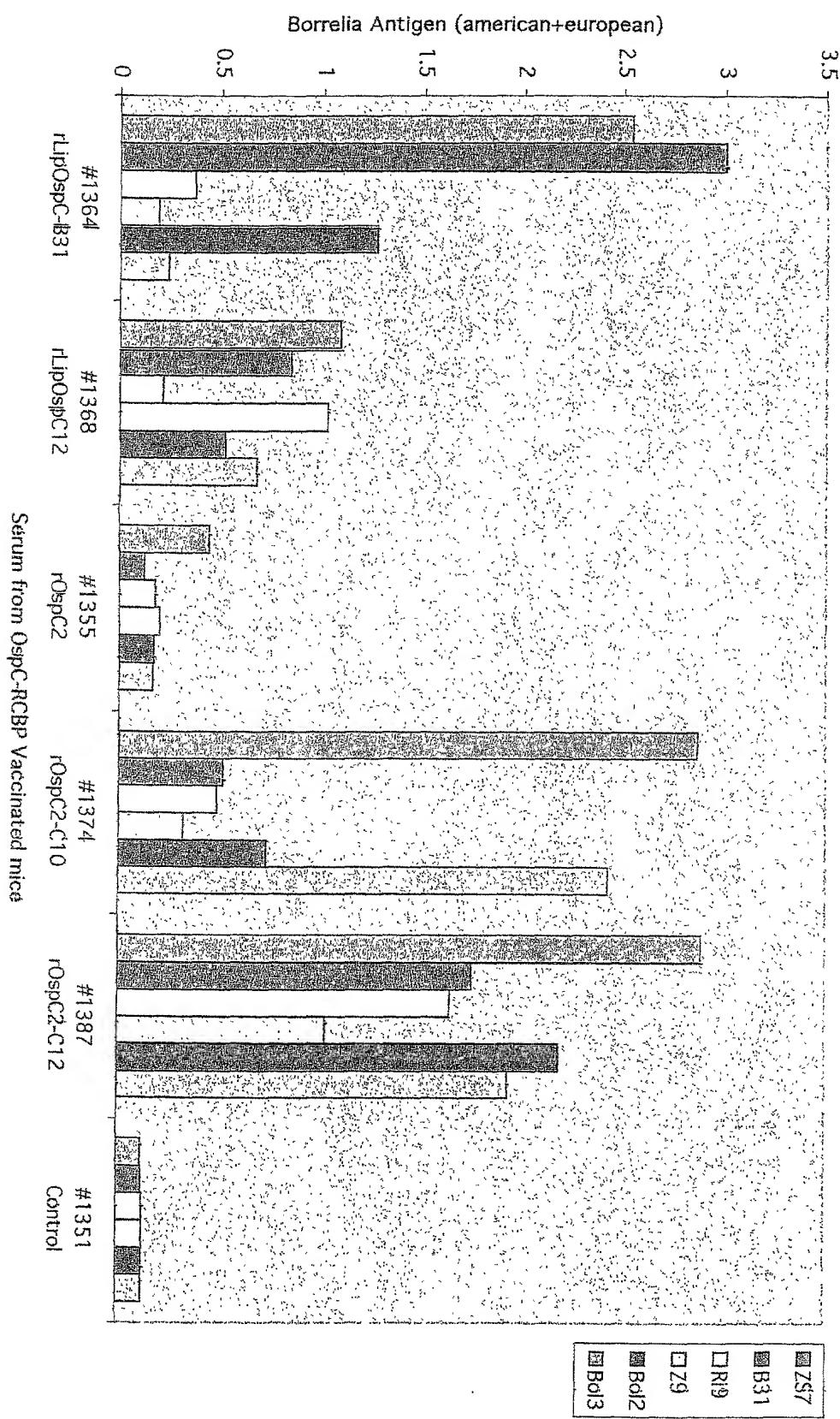


Fig. 5

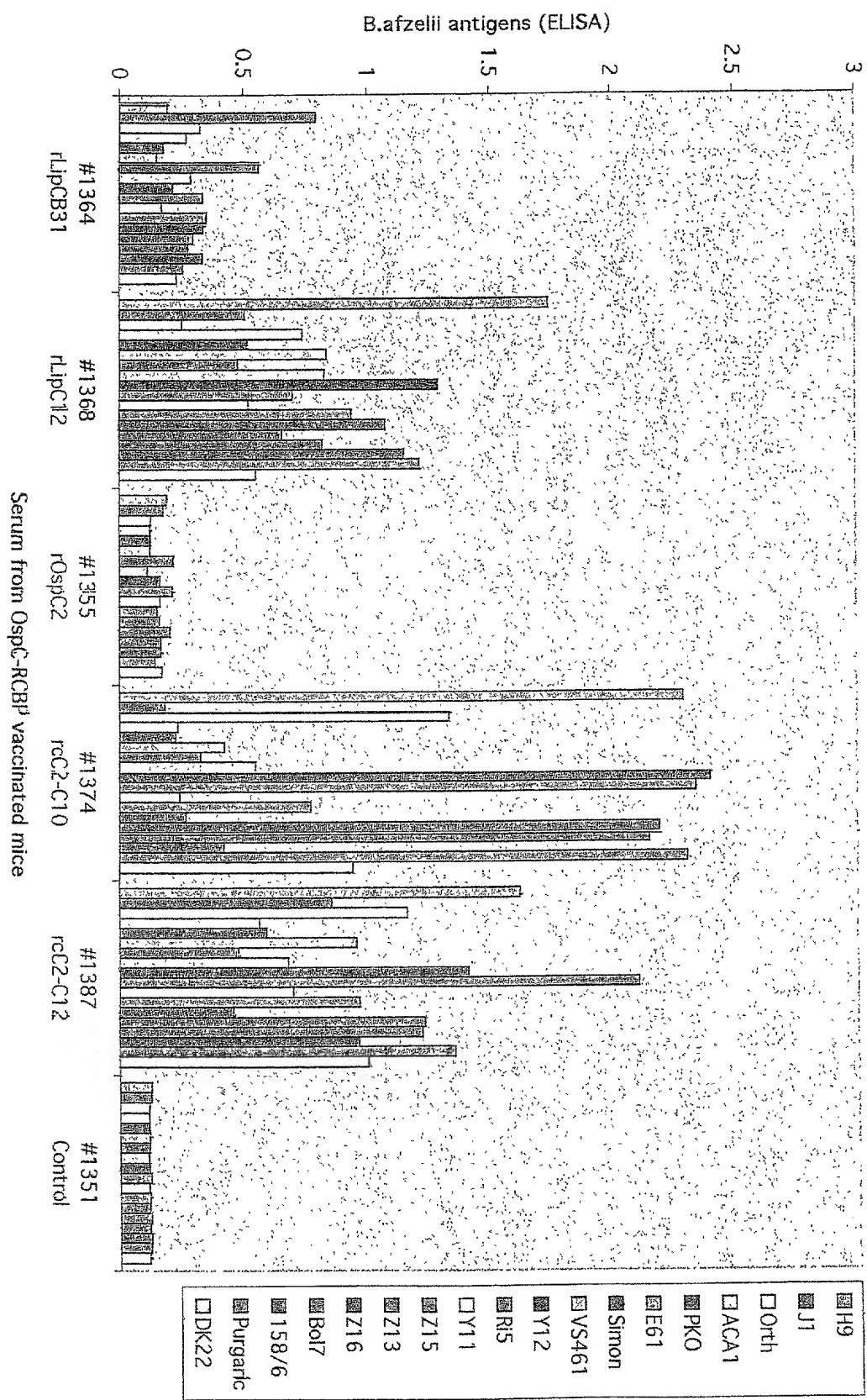
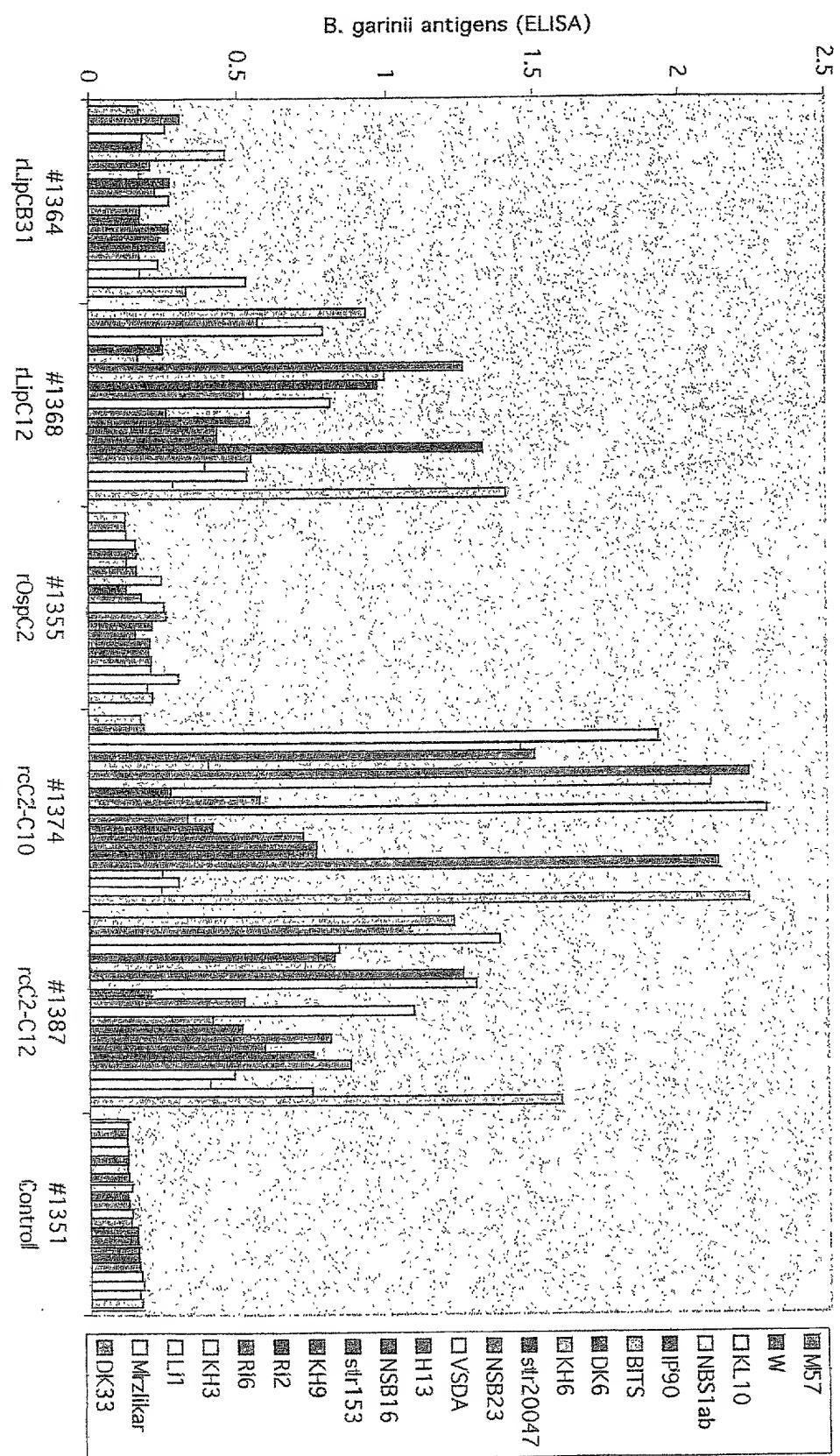


Fig. 6



Early Lyme: #P(total)				Sensitivity		Potential cross-reactivity: #P(Total Tested)			Specificity		
EMA	EA	Ac. Dissem.	Ac. Convål.	#P(Total)	(%)	Syphilis	SLE & RA	Normals End.	Normals NonEnd.	#P(Total)	(%)
C1 (chrt1)	6(10)	ND	4(10)	8(8)	18(28)	64%	1(10)	2(10)	0(8)	4(38)	11%
C2 (chrt2)	4(10)	ND	5(10)	8(8)	17(28)	61%	0(10)	2(10)	0(8)	4(38)	11%
C1C10 (chrt3)	7(10)	ND	4(10)	5(8)	16(28)	57%	4(10)	1(10)	2(10)	0(8)	7(38)
C1C12 (chrt4)	2(10)	ND	3(10)	5(8)	10(28)	36%	2(10)	0(10)	0(10)	ND	2(30)
B31C10 (chrt5)	8(10)	ND	6(10)	5(8)	19(28)	68%	2(10)	2(10)	4(10)	0(8)	8(38)
B31C12 (chrt6)	7(10)	ND	6(10)	6(8)	19(28)	68%	1(10)	1(10)	1(10)	0(8)	3(38)
C2C7 (chrt7)	5(10)	6(8)	3(10)	4(7)	18(35)	51%	1(11)	0(10)	1(20)	0(8)	2(49)
C2C10 (chrt8)	4(10)	7(8)	5(10)	4(7)	20(35)	57%	0(11)	0(10)	1(20)	0(8)	1(49)
C2C12 (chrt9)	5(10)	7(8)	6(10)	4(7)	22(35)	63%	0(11)	1(10)	3(20)	0(8)	4(49)
C5C7 (chrt10)	7(10)	ND	4(10)	5(8)	16(28)	57%	2(10)	2(10)	0(10)	ND	4(30)
C5C10 (chrt11)	6(10)	ND	4(10)	5(8)	15(28)	54%	0(10)	0(10)	0(10)	ND	0(30)
C5C12 (chrt12)	8(10)	ND	8(10)	6(8)	22(28)	79%	5(10)	3(10)	0(8)	11(38)	29%

EMA = Erythema Migrans Acute

EA = Acute Disseminated

Ac. Dissem.= Acute Disseminated

Ac. Convål. = Acute Convalescent

#P = Number of positives

SLE = Systemic Lupus Erythematosus

RA = Rheumatoid Arthritis

End. = Endemic Field Workers

NonEnd. = Non Endemic

Fig. 8

SEQUENCE LISTING

<110> Dattwyler, Raymond J.
 Seinost, Gerald
 Dykhuizen, Danial
 Luft, Benjamin J.
 Maria J.C. Gomes-Solecki

<120> Groups of *Borrelia burgdorferi* and
Borrelia afzelii That Cause Lyme Disease in Humans

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 85 90 95
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 Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala
 130 135 140
 Lys Lys Ala Ile Leu Lys Ala Asn Ala Gly Lys Asp Lys Gly Val
 145 150 155 160
 Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala
 165 170 175
 Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val
 180 185 190
 Val

<210> 13

<211> 576

<212> DNA

<213> Borrelia burgdorferi

<220>

<221> CDS

<222> (1)...(576)

<400> 13

atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg 48
 Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
 1 5 10 15

aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45

gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192
 Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
 50 55 60

aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc aat cag 240
 Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
 65 70 75 80

agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta	288
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu	
85 90 95	
ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag	336
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys	
100 105 110	
att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa	384
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys	
115 120 125	
agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca	432
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala	
130 135 140	
caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca	480
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala	
145 150 155 160	
gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct	528
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala	
165 170 175	
caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg	576
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val	
180 185 190	

<210> 14
<211> 191
<212> PRT
<213> Borrelia burgdorferi

<400> 14

Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn	
1 5 10 15	
Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr	
20 25 30	
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val	
35 40 45	
Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys	
50 55 60	
Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser	
65 70 75 80	
Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile	
85 90 95	
Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile	
100 105 110	
Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser	
115 120 125	
Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln	
130 135 140	
Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu	
145 150 155 160	
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln	
165 170 175	

Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
180 185 190

<210> 15
<211> 576
<212> DNA
<213> borrelia burgdorferi

<220>
<221> CDS
<222> (1) ... (576)

<400> 15

atg act tta ttt tta ttt ata tct tgt aat aat tca aga aaa gat ggg	48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Arg Lys Asp Gly	
1 5 10 15	

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aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt 96
Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
          20           25           30

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aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc      144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
          35           40           45

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gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc   192
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
      50          55          60

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aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag 240
Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
65 70 75 80

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agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta    288
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu
                      85          90          95

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ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag      336
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys
          100           105           110

```

att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa 384
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys
115 120 125

```

agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca      432
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala
   130          135          140

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caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca      480
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
145          150          155          160

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gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528
 Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
 165 170 175

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576
 Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
 180 185 190

<210> 16
 <211> 191
 <212> PRT
 <213> borrelia burgdorferi

<400> 16
 Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Arg Lys Asp Gly Asn
 1 5 10 15
 Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
 20 25 30
 Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
 35 40 45
 Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
 50 55 60
 Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser
 65 70 75 80
 Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile
 85 90 95
 Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile
 100 105 110
 Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser
 115 120 125
 Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln
 130 135 140
 Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu
 145 150 155 160
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln
 165 170 175
 Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
 180 185 190

<210> 17
 <211> 573
 <212> DNA
 <213> Borrelia burgdorferi

<220>
 <221> CDS
 <222> (1)...(573)

<400> 17
 atg act tta ttt tta ttt ata tct tgt aat aat tca ggg aaa gat ggg 48
 Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
 1 5 10 15
 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30
 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45

gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys 50 55 60	192
gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala 65 70 75 80	240
gat cac aac gga tca tta ata tca gga gca tat tta att tca aac tta Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu 85 90 95	288
ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala 100 105 110	336
gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu 115 120 125	384
aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn 130 135 140	432
gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc gct Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala 145 150 155 160	480
gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala 165 170 175	528
gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc cct Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro 180 185 190	573

<210> 18
<211> 190
<212> PRT
<213> Borrelia burgdorferi

<400> 18

Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn 1 5 10 15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr 20 25 30
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val 35 40 45
Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala 50 55 60
Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp 65 70 75 80
His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile 85 90 95
Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu 100 105 110

Ile	Glu	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys
		115					120				125				
Gly	Glu	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn	Ala
		130				135				140					
Lys	Lys	Ala	Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala	Asp
		145			150					155					160
Glu	Leu	Glu	Lys	Leu	Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala	Ala
					165			170							175
Lys	Glu	Met	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro		
			180				185				190				

<210> 19
<211> 553
<212> DNA
<213> *Borrelia burgdorferi*

<220>
<221> CDS
<222> (1) ... (553)

<400> 19
 atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg 48
 Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
 1 5 10 15

 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30

 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45

 gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act 192
 Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
 50 55 60

 aaa gct att ggt aaa aaa ata gat aac aat gct ggt ttg ggt gct gaa 240
 Lys Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu
 65 70 75 80

 gtg ggt caa aac gga tca ttg cta gca gga gct tat gca atc tca act 288
 Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
 85 90 95

 gta ata ata gaa aaa ttg agc aca tta aaa aat gta gaa gaa tta aaa 336
 Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys
 100 105 110

 gaa aaa att aca aag gct aag gat tgt tct gaa aaa ttc act aaa aaa 384
 Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys
 115 120 125

 tta aaa gat agc cgc gca gag ctt ggt aaa aaa gat gcc agt gat gat 432
 Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp
 130 135 140

gat gca aaa aaa gct att tta aaa aca aat caa gct aac gat aag ggt	480
Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly	
145 150 155 160	
gct aaa gaa ctt aaa gag tta ttt gaa gca gta gaa agc ttg tca aaa	528
Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys	
165 170 175	
gcg gct aaa gag atg cta aac aag t	553
Ala Ala Lys Glu Met Leu Asn Lys	
180	

<210> 20
<211> 183
<212> PRT
<213> Borrelia burgdorferi

<400> 20	
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn	
1 5 10 15	
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr	
20 25 30	
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val	
35 40 45	
Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys	
50 55 60	
Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu Val	
65 70 75 80	
Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Val	
85 90 95	
Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys Glu	
100 105 110	
Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys Leu	
115 120 125	
Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp Asp	
130 135 140	
Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly Ala	
145 150 155 160	
Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys Ala	
165 170 175	
Ala Lys Glu Met Leu Asn Lys	
180	

<210> 21
<211> 582
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(582)

<400> 21	
atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg	48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly	
1 5 10 15	

aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu 20 25 30	96
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala 35 40 45	144
gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr 50 55 60	192
aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa Lys Ala Ile Gly Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu 65 70 75 80	240
gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca aaa Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys 85 90 95	288
cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys 100 105 110	336
gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys 115 120 125	384
cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat gag Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu 130 135 140	432
aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag ggc Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly 145 150 155 160	480
gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys 165 170 175	528
gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agt cct Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro 180 185 190	576
att gtg Ile Val	582

<210> 22
<211> 193
<212> PRT
<213> Borrelia burgdorferi

<400> 22
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
1 5 10 15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30

Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
 35 40 45
 Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
 50 55 60
 Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala
 65 70 75 80
 Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu
 85 90 95
 Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu
 100 105 110
 Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu
 115 120 125
 Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn
 130 135 140
 Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala
 145 150 155 160
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala
 165 170 175
 Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Ile
 180 185 190
 Val

<210> 23
 <211> 1128
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1128)

<400> 23
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 85 90 95	288
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 100 105 110	336
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 115 120 125	384
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 130 135 140	432
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala 180 185 190	576
atg gta aat aat tca ggg aaa gat ggg aat aca tct gca aat tct gct Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala 195 200 205	624
gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile 210 215 220	672
aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu 225 230 235 240	720
ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata aaa Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys 245 250 255	768
aac gat gtt agt tta gat aat gag gca gat cac aac gga tca tta ata Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile 260 265 270	816
tca gga gca tat tta att tca aac tta ata aca aaa aaa ata agt gca Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala 275 280 285	864
ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct aag aaa Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys 290 295 300	912
tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca gat ctt Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu 305 310 315 320	960

ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att tta aaa		1008
Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys		
325	330	335
aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag tta ttt		1056
Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe		
340	345	350
gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt act aat		1104
Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn		
355	360	365
tca gtt aaa gag ctt aca agc taa		1128
Ser Val Lys Glu Leu Thr Ser *		
370	375	

<210> 24
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 24			
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala			
1	5	10	15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile			
20	25	30	
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu			
35	40	45	
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile			
50	55	60	
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu			
65	70	75	80
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp			
85	90	95	
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys			
100	105	110	
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu			
115	120	125	
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys			
130	135	140	
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe			
145	150	155	160
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn			
165	170	175	
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met			
180	185	190	
Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp			
195	200	205	
Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr			
210	215	220	
Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu			
225	230	235	240
Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn			
245	250	255	

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<210> 25
<211> 1124
<212> DNA
<213> Artificial Sequence
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<220>
<223> OspC Chimera

<221> CDS
<222> (1) ... (1124)

<400> 25
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa      96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
          20           25           30

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att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

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ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa      192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
      50           55           60

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ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca	240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 115 120 125	384
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 130 135 140	432
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala 180 185 190	576
atg gta aat aat tca gga aaa gat ggg aat aca tct gca aat tct gct Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala 195 200 205	624
gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile 210 215 220	672
aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu 225 230 235 240	720
ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa aaa ata Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile 245 250 255	768
caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu 260 265 270	816
tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa tta gat Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp 275 280 285	864
gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat gct aag Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys 290 295 300	912
aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat gcg caa Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln 305 310 315 320	960
ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct att tta Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu 325 330 335	1008
ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa aag cta Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu 340 345 350	1056

ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg ctt gct 1104
 Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala
 355 360 365

aat tca gtt aaa gag ctt ac 1124
 Asn Ser Val Lys Glu Leu
 370

<210> 26
 <211> 373
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 26
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 1 5 10 15
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 20 25 30
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 35 40 45
 Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60
 His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu
 65 70 75 80
 Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
 85 90 95
 Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
 115 120 125
 Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
 130 135 140
 Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
 145 150 155 160
 Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
 165 170 175
 Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met
 180 185 190
 Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp
 195 200 205
 Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr
 210 215 220
 Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu
 225 230 235 240
 Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln
 245 250 255
 Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu
 260 265 270
 Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly
 275 280 285
 Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys
 290 295 300
 Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu
 305 310 315 320

Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile
 325 330 335
 Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 340 345 350
 Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn
 355 360 365
 Ser Val Lys Glu Leu
 370

<210> 27
<211> 1137
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1) . . . (1137)

<400> 27
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
 20 25 30
 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65 70 75 80
 ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys 180 185 190	576
aaa cct tcc atg gta aat aat tca ggg aaa gat ggg aat aca tct gca Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala 195 200 205	624
aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser 210 215 220	672
aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val 225 230 235 240	720
gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys 245 250 255	768
aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly 260 265 270	816
tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys 275 280 285	864
ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys 290 295 300	912
gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His 305 310 315 320	960
aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala 325 330 335	1008
att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu 340 345 350	1056
aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met 355 360 365	1104
ctt act aat tca gtt aaa gag ctt aca agc taa Leu Thr Asn Ser Val Lys Glu Leu Thr Ser *	1137
370 375	

<210> 28
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 28
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
180 185 190
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
195 200 205
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
210 215 220
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
225 230 235 240
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
245 250 255
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
260 265 270
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
275 280 285
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
290 295 300
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
305 310 315 320
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
325 330 335
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
340 345 350
Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
355 360 365
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
370 375

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<210> 29
<211> 1133
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1133)

<400> 29
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175

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aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
180	185
190	
aaa cct tcc atg gta aat aat tca gga aaa gat ggg aat aca tct gca	624
Lys Pro Ser Met Val Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala	
195	200
205	
aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt	672
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser	
210	215
220	
aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att	720
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile	
225	230
235	240
gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt	768
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly	
245	250
255	
aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat	816
Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn	
260	265
270	
gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa	864
Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln	
275	280
285	
aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa	912
Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu	
290	295
300	
aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa	960
Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu	
305	310
315	320
cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa	1008
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys	
325	330
335	
gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt	1056
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu	
340	345
350	
gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag	1104
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu	
355	360
365	
atg ctt gct aat tca gtt aaa gag ctt ac	1133
Met Leu Ala Asn Ser Val Lys Glu Leu	
370	375

<210> 30
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 30
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
180 185 190
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
195 200 205
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
210 215 220
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
225 230 235 240
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
245 250 255
Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn
260 265 270
Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln
275 280 285
Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu
290 295 300
Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu
305 310 315 320
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
325 330 335
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
340 345 350
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
355 360 365
Met Leu Ala Asn Ser Val Lys Glu Leu
370 375

<210> 31
<211> 1112
<212> DNA
<213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS

<222> (1)...(1112)

<400> 31

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct	48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile	
50 55 60	

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg	240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
65 70 75 80	

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt	288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser	
85 90 95	

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag	336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys	
100 105 110	

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag	384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln	
115 120 125	

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta	432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	
130 135 140	

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag	480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys	
145 150 155 160	

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt	528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu	
165 170 175	

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat	576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn	
180 185 190	

tca aga aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt	624
Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val	
195 200 205	

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac		672	
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn			
210	215	220	
gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata		720	
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile			
225	230	235	240
gat gaa ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt		768	
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly			
245	250	255	
tta gag gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat		816	
Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr			
260	265	270	
gca ata tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa		864	
Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu			
275	280	285	
gaa tta aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt		912	
Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe			
290	295	300	
act aat aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt		960	
Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu			
305	310	315	320
act gat gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa		1008	
Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys			
325	330	335	
gat aag ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac		1056	
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn			
340	345	350	
tta tca aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt		1104	
Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu			
355	360	365	
aca agt cc		1112	
Thr Ser			
370			

<210> 32
<211> 369
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 32
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30

Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 35 40 45
 Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
 50 55 60
 Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
 65 70 75 80
 Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
 85 90 95
 Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
 115 120 125
 Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
 130 135 140
 Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
 145 150 155 160
 Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
 180 185 190
 Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys
 195 200 205
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 210 215 220
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp
 225 230 235 240
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu
 245 250 255
 Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala
 260 265 270
 Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu
 275 280 285
 Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr
 290 295 300
 Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr
 305 310 315 320
 Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp
 325 330 335
 Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu
 340 345 350
 Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr
 355 360 365
 Ser

<210> 33
 <211> 1113
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1113)

<400> 33

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser 1 5 10 15	48
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 20 25 30	96
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 35 40 45	144
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile 50 55 60	192
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 65 70 75 80	240
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser 85 90 95	288
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys 100 105 110	336
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln 115 120 125	384
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu 130 135 140	432
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys 145 150 155 160	480
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu 165 170 175	528
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn 180 185 190	576
tca ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val 195 200 205	624
aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn 210 215 220	672
gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile 225 230 235 240	720

gat gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt		768	
Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser			
245	250	255	
tta gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat		816	
Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr			
260	265	270	
tta att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca		864	
Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser			
275	280	285	
gga gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa		912	
Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu			
290	295	300	
ttt act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc		960	
Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly			
305	310	315	320
gtt act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat		1008	
Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp			
325	330	335	
aaa act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa		1056	
Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys			
340	345	350	
aac ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag		1104	
Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu			
355	360	365	
ctt aca agc		1113	
Leu Thr Ser			
370			

<210> 34
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 34
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
50 55 60
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
65 70 75 80
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
85 90 95

Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
 115 120 125
 Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
 130 135 140
 Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
 145 150 155 160
 Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
 180 185 190
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 195 200 205
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 210 215 220
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
 225 230 235 240
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
 245 250 255
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
 260 265 270
 Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
 275 280 285
 Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
 290 295 300
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
 305 310 315 320
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
 325 330 335
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
 340 345 350
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
 355 360 365
 Thr Ser
 370

<210> 35
 <211> 1112
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1112)

<400> 35
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 35 40 45	144
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile 50 55 60	192
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 65 70 75 80	240
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser 85 90 95	288
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys 100 105 110	336
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln 115 120 125	384
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu 130 135 140	432
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys 145 150 155 160	480
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu 165 170 175	528
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn 180 185 190	576
tca gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val 195 200 205	624
aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn 210 215 220	672
gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile 225 230 235 240	720
gat gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly 245 250 255	768
ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala 260 265 270	816

tat aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat		864
Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn		
275	280	285
tca gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa		912
Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu		
290	295	300
gat ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa		960
Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu		
305	310	315
aat gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca		1008
Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala		
325	330	335
gct aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta		1056
Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val		
340	345	350
gaa aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa		1104
Glu Asn Leu Ala Lys Ala Lys Glu Met Leu Ala Asn Ser Val Lys		
355	360	365
gag ctt ac		1112
Glu Leu		
370		
<210> 36		
<211> 369		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> OspC Chimera		
<400> 36		
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala		
1 5 10 15		
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile		
20 25 30		
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu		
35 40 45		
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys		
50 55 60		
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu		
65 70 75 80		
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys		
85 90 95		
Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys Lys		
100 105 110		
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu		
115 120 125		
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys		
130 135 140		
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu		
145 150 155		160

Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
 180 185 190
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 195 200 205
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 210 215 220
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp
 225 230 235 240
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly
 245 250 255
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr
 260 265 270
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser
 275 280 285
 Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
 290 295 300
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
 305 310 315 320
 Val Thr Asp Glu Asn Ala Lys Ala Ile Leu Ile Thr Asp Ala Ala
 325 330 335
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
 340 345 350
 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
 355 360 365
 Leu

<210> 37
 <211> 1106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1106)

<400> 37
 atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu 65 70 75 80	240
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat Leu Ser Gly Ala Tyr Ala Ser Asp Leu Ile Ala Glu Lys Leu Asn 85 90 95	288
gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln 100 105 110	336
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu 115 120 125	384
ggc ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys 130 135 140	432
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe 145 150 155 160	480
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn 165 170 175	528
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca aga Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg 180 185 190	576
aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly 195 200 205	624
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val 210 215 220	672
gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu 225 230 235 240	720
ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu 245 250 255	768
gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile 260 265 270	816
tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu 275 280 285	864
aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn 290 295 300	912

aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat		960
Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp		
305	310	315
320		
gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag		1008
Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys		
325	330	335
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser		
340	345	350
aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt		1056
Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser		
355	360	365

cc 1106

<210> 38
<211> 368
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 38
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
50 55 60
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65 70 75 80
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
85 90 95
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
100 105 110
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
115 120 125
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
130 135 140
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145 150 155 160
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
165 170 175
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg
180 185 190
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly
195 200 205
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
210 215 220
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu
225 230 235 240

Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Ile	Gly	Asn	Asn	Gly	Leu	Glu	
			245					250					255		
Ala	Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu	Leu	Ser	Gly	Ala	Tyr	Ala	Ile
			260					265					270		
Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn	Val	Leu	Lys	Asn	Glu	Glu	Leu
			275				280					285			
Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln	Cys	Ser	Thr	Glu	Phe	Thr	Asn
			290			295					300				
Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu	Gly	Leu	Asp	Asn	Leu	Thr	Asp
				310					315					320	
Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys	Lys	His	Ala	Asn	Lys	Asp	Lys
				325				330					335		
Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu	Ser
			340					345					350		
Lys	Ala	Ala	Gln	Asp	Thr	Leu	Lys	Asn	Ala	Val	Lys	Glu	Leu	Thr	Ser
			355				360					365			

<210> 39
<211> 1107
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1) ... (1107)

<400> 39
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att aca gaa tct aac gca gtt ctg gcc gtg aaa gaa gtt gag acc 144
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60

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ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
   65           70           75           80

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tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85 90 95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
 100 105 110

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt		384	
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu			
115	120	125	
ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa		432	
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys			
130	135	140	
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt		480	
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe			
145	150	155	160
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat		528	
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn			
165	170	175	
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca ggg		576	
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly			
180	185	190	
aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg		624	
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly			
195	200	205	
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt		672	
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val			
210	215	220	
gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag		720	
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu			
225	230	235	240
ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat		768	
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp			
245	250	255	
aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta att		816	
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile			
260	265	270	
tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa		864	
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu			
275	280	285	
ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act		912	
Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr			
290	295	300	
gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act		960	
Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr			
305	310	315	320
gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act		1008	
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr			
325	330	335	
aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg		1056	
Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu			
340	345	350	

tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca	1104
Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr	
355	360

agc	1107
Ser	

<210> 40
<211> 368
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 40	
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser Ala	
1 5 10 15	
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile	
20 25 30	
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu	
35 40 45	
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile	
50 55 60	
Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu	
65 70 75 80	
Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val	
85 90 95	
Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys	
100 105 110	
Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly	
115 120 125	
Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys	
130 135 140	
His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys	
145 150 155 160	
Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala	
165 170 175	
Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly Lys	
180 185 190	
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
195 200 205	
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val	
210 215 220	
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu	
225 230 235 240	
Ala Lys Ala Ile Gly Lys Ile Lys Asn Asp Val Ser Leu Asp Asn	
245 250 255	
Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser	
260 265 270	
Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu	
275 280 285	
Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala	
290 295 300	
Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
305 310 315 320	

Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys
				325				330						335	
Gly	Ala	Asp	Glu	Leu	Glu	Lys	Leu	Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser
			340				345						350		
Lys	Ala	Ala	Lys	Glu	Met	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser
			355				360					365			

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<210> 41
<211> 1106
<212> DNA
<213> Artificial Sequence
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<220>
<223> OspC Chimera

<221> CDS
<222> (1) ... (1106)

<400> 41
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15

```

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
          20           25           30

```

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45

```

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa      192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
      50           55           60

```

```

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65           70           75           80

```

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85 90 95

```

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa      336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
          100           105           110

```

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 115 120 125

```

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
    130           135           140

```

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe 145 150 155 160	480
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn 165 170 175	528
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca gga Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly 180 185 190	576
aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly 195 200 205	624
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val 210 215 220	672
gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu 225 230 235 240	720
ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu 245 250 255	768
gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr 260 265 270	816
ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu 275 280 285	864
aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe 290 295 300	912
act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val 305 310 315 320	960
act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys 325 330 335	1008
gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn 340 345 350	1056
ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu 355 360 365	1104
ac	1106

<211> 367
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 42

Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Ala	Ser	Ala	Asn	Ser	Ala
1				5				10				15			
Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile
				20				25				30			
Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu
				35			40				45				
Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile
				50			55				60				
Gly	Asn	Asn	Gly	Leu	Glu	Ala	Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu	Leu
				65			70			75				80	
Ser	Gly	Ala	Tyr	Ala	Ile	Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn	Val
				85				90				95			
Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu	Ile	Asp	Thr	Ala	Lys	Gln	Cys	
				100			105				110				
Ser	Thr	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu	Gly
				115			120				125				
Leu	Asp	Asn	Leu	Thr	Asp	Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys	Lys
				130			135			140					
His	Ala	Asn	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys
				145			150			155				160	
Ala	Val	Glu	Asn	Leu	Ser	Lys	Ala	Ala	Gln	Asp	Thr	Leu	Lys	Asn	Ala
				165				170				175			
Val	Lys	Glu	Leu	Thr	Ser	Pro	Ile	Val	His	Gly	Asn	Asn	Ser	Gly	Lys
				180				185				190			
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro
				195				200				205			
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val
				210			215				220				
Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu
				225			230			235				240	
Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	Leu	Ala
				245				250				255			
Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile
				260				265				270			
Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	Glu	Lys
				275			280				285				
Leu	Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe	Thr
				290			295				300				
Lys	Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile	Glu	Asn	Val	Thr
				305			310			315				320	
Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp	Ala	Ala	Lys	Asp
				325				330				335			
Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu
				340				345				350			
Ala	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	
				355			360				365				

<210> 43
<211> 633
<212> DNA

<213> Borrelia burgdorferi

<220>

<221> CDS

<222> (1)...(633)

<400> 43

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atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
   1           5           10          15

```

48

ata tct tgt aat aat tca ggg aaa gat	ggg aat aca tct gca aat tct	
Ile Ser Cys Asn Asn Ser Gly Lys Asp	Gly Asn Thr Ser Ala Asn Ser	
20	25	30

96

```

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
          35           40           45

```

144

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcc
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 50 55 60

192

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
65 70 75 80

240

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
85 90 95

288

```

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tt
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Le
          100           105           110

```

336

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aac
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Ly
 115 120 125

384

```

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca ga
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr As
    130          135          140

```

432

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tt
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Le
 145 150 155 160

480

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tt
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Le
165 170 175

528

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gc
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Al
180 185 190

576

```

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aa
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ly
          105           200           205

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624

aaa cct taa		633
Lys Pro *		
210		

<210> 44
<211> 209
<212> PRT
<213> Borrelia burgdorferi

<400> 44

Lys	Lys	Asn	Thr	Leu	Ser	Ala	Ile	Leu	Met	Thr	Leu	Phe	Leu	Phe	Ile
1				5				10						15	
Ser	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala
				20				25						30	
Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Asn	Lys	Lys	Ile
				35				40					45		
Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu
				50				55				60			
Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile
				65				70			75			80	
His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Asn	Asn	His	Asn	Gly	Ser	Leu
				85				90					95		
Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp
				100				105					110		
Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys
				115				120				125			
Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu
				130				135			140				
Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys
				145				150			155			160	
Ala	Asn	Gly	Thr	Lys	Thr	Lys	Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe
				165				170				175			
Glu	Ser	Val	Glu	Val	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn
				180				185				190			
Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys
				195				200				205			
Pro															

<210> 45
<211> 580
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(580)

<400> 45

atg	gct	tgt	aat	aat	tca	ggg	aaa	gat	ggg	aat	aca	tct	gca	aat	tct
1					5										48
Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser
													15		
gct	gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	aat	aaa	aaa
														96	
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Asn	Lys	Lys
					20				25			30			

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 35 40 45	144
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys 50 55 60	192
ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser 65 70 75 80	240
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 85 90 95	288
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 100 105 110	336
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 115 120 125	384
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 130 135 140	432
aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Ala Asn Gly Thr Lys Thr Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca tcc Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser 180 185 190	576
atg g Met	580

<210> 46
<211> 192
<212> PRT
<213> Borrelia burgdorferi

<400> 46
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60

His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser Leu
 65 70 75 80
 Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
 85 90 95
 Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
 115 120 125
 Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
 130 135 140
 Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
 145 150 155 160
 Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
 165 170 175
 Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser Met
 180 185 190

<210> 47

<211> 639

<212> DNA

<213> Borrelia garinii

<220>

<221> CDS

<222> (1)...(639)

<400> 47

atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt	48
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe	
1 5 10 15	

ata tct tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat	96
Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn	
20 25 30	

cct gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa	144
Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
35 40 45	

aaa att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag	192
Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu	
50 55 60	

act ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa	240
Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln	
65 70 75 80	

aaa ata gac aat aat ggt tta gct gct tta aat aat cag aat gga	288
Lys Ile Asp Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly	
85 90 95	

tcg ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa	336
Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys	
100 105 110	

ttg agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag	384
Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys	
115 120 125	

gct aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat	432
Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His	
130 135 140	
gca gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct	480
Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala	
145 150 155 160	
att tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa	528
Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys	
165 170 175	
gat tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca	576
Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala	
180 185 190	
cta act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt	624
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser	
195 200 205	
cca aaa aaa cct taa	639
Pro Lys Lys Pro *	
210	

<210> 48
<211> 211
<212> PRT
<213> Borrelia garinii

<400> 48
Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
1 5 10 15
Ser Cys Ser Asn Ser Gly Lys Gly Asp Ser Ala Ser Thr Asn Pro
20 25 30
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
35 40 45
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
50 55 60
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
65 70 75 80
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
85 90 95
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
100 105 110
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
115 120 125
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
130 135 140
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
145 150 155 160
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
165 170 175
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
180 185 190
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
195 200 205

Lys Lys Pro
210

<210> 49
<211> 624
<212> DNA
<213> *Borrelia afzelii*

<220>
<221> CDS
<222> (1)...(624)

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<400> 49
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Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
   1           5           10          15

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ata tct tgt aat aat tca ggt ggg gat tct gca tct act aat cct gat 96
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp
          20           25           30

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gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa att aca 144
 Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr
 35 40 45

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gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt 192
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu
      50           55           60

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tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat	240
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn	
65 70 75 80	

gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg ata gca 288
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala
85 90 95

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gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt gta ttg 336
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu
          100           105           110

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aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat tgt tcc 384
Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser
115 120 125

caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt ggt ata 432
 Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile
 130 135 140

caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa aca cat 480
 Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His
 145 150 155 160

gga act aaa gag aag ggt gct aaa gaa ctt gaa gag tca ccc aaa tca 528
 Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser
 165 170 175

cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat tca gtt 576
 Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val
 180 185 190

aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 624
 Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
 195 200 205

<210> 50
 <211> 206
 <212> PRT
 <213> Borrelia afzelii

<400> 50
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 Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu
 20 25 30
 Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp
 35 40 45
 Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser
 50 55 60
 Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp
 65 70 75 80
 Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly
 85 90 95
 Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn
 100 105 110
 Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln
 115 120 125
 Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln
 130 135 140
 Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly
 145 150 155 160
 Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu
 165 170 175
 Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys
 180 185 190
 Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 195 200 205

<210> 51
 <211> 1680
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 <213> ospC Chimera

<220>
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 1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 20 25 30	96
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 35 40 45	144
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys 50 55 60	192
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser 65 70 75 80	240
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 85 90 95	288
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 100 105 110	336
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 115 120 125	384
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 130 135 140	432
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala 180 185 190	576
atg ggt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro 195 200 205	624
gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 210 215 220	672
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr 225 230 235 240	720
ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys 245 250 255	768

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser 260	265	270	816	
ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg Leu Leu Ala Gly Ala Tyr Ala Ser Thr Leu Ile Thr Glu Lys Leu 275	280	285	864	
agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala 290	295	300	912	
aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala 305	310	315	320	960
gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile 325	330	335	1008	
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp 340	345	350	1056	
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu 355	360	365	1104	
act aat tca gtt aaa gaa ctt ggt cac cgt aat aat tca ggt ggg gat Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp 370	375	380	1152	
tct gca tct act aat cct gat gag tct gca aaa gga cct aat ctt acc Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr 385	390	395	400	1200
gta ata agc aaa aaa att aca gat tct aat gca ttt tta ctg gct gtg Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val 405	410	415	1248	
aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt tct aaa gct Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala 420	425	430	1296	
att ggt aaa aaa ata aaa aat gat ggt act tta gat aac gaa gca aat Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn 435	440	445	1344	
cga aac gaa tca ttg ata gca gga gct tat gaa ata tca aaa cta ata Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile 450	455	460	1392	
aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag aaa aaa att Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile 465	470	475	480	1440

aaa gag gct aag gat tgt tcc caa aaa ttt act act aag cta aaa gat		1488
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp		
485	490	495
agt cat gca gag ctt ggt ata caa agc gtt cag gat gat aat gca aaa		1536
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys		
500	505	510
aaa gct att tta aaa aca cat gga act aaa gac aag ggt gct aaa gaa		1584
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu		
515	520	525
ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa		1632
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln		
530	535	540
gca gca tta act aat tca gtt aaa gag ctt aca aat cct gtt gtg gca		1680
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala		
545	550	555
		560

<210> 52
<211> 560
<212> PRT
<213> ospC Chimera

<400> 52

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser			
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys			
20	25	30	
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala			
35	40	45	
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys			
50	55	60	
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser			
65	70	75	80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu			
85	90	95	
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys			
100	105	110	
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp			
115	120	125	
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu			
130	135	140	
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu			
145	150	155	160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala			
165	170	175	
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala			
180	185	190	
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro			
195	200	205	
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys			
210	215	220	
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr			
225	230	235	240

Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
 245 250 255
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
 260 265 270
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
 275 280 285
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
 290 295 300
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
 305 310 315 320
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
 325 330 335
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
 340 345 350
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
 355 360 365
 Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp
 370 375 380
 Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr
 385 390 395 400
 Val Ile Ser Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val
 405 410 415
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala
 420 425 430
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn
 435 440 445
 Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile
 450 455 460
 Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile
 465 470 475 480
 Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp
 485 490 495
 Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys
 500 505 510
 Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu
 515 520 525
 Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln
 530 535 540
 Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala
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 <211> 1137
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1137)

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 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 35 40 45	144
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile 50 55 60	192
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 65 70 75 80	240
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser 85 90 95	288
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys 100 105 110	336
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln 115 120 125	384
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu 130 135 140	432
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys 145 150 155 160	480
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu 165 170 175	528
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn 180 185 190	576
tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly 195 200 205	624
cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe 210 215 220	672
tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu 225 230 235 240	720
ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp 245 250 255	768

aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile 260 265 270	816
tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu 275 280 285	864
aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr 290 295 300	912
aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp 305 310 315 320	960
gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag Asp Asn Ala Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys 325 330 335	1008
ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser 340 345 350	1056
aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn 355 360 365	1104
cct gtt gtg gca gaa agt cca aaa aaa cct taa Pro Val Val Ala Glu Ser Pro Lys Lys Pro *	1137
370 375	
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<211> 378	
<212> PRT	
<213> ospC Chimera	
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 20 25 30	
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 35 40 45	
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile 50 55 60	
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 65 70 75 80	
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser 85 90 95	
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys 100 105 110	
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln 115 120 125	
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu 130 135 140	
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys 145 150 155 160	

Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180 185 190
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
 195 200 205
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 210 215 220
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
 225 230 235 240
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
 245 250 255
 Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
 260 265 270
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
 275 280 285
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
 290 295 300
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
 305 310 315 320
 Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
 325 330 335
 Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
 340 345 350
 Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
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 Pro Val Val Ala Glu Ser Pro Lys Lys Pro
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 <211> 1158
 <212> DNA
 <213> ospC Chimera

<220>
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 <222> (1)...(1158)

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 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60

 ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 85 90 95	288
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 100 105 110	336
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 115 120 125	384
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 130 135 140	432
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys 180 185 190	576
aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat Lys Pro Phe His Gly Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn 195 200 205	624
cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys 210 215 220	672
att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala 225 230 235 240	720
ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile 245 250 255	768
aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 260 265 270	816
ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser 275 280 285	864
gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp 290 295 300	912

tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt	960
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu	
305 310 315 320	
ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa	1008
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys	
325 330 335	
aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt	1056
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe	
340 345 350	
aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat	1104
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn	
355 360 365	
tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa	1152
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys	
370 375 380	
cct taa	1158
Pro *	
385	

<210> 56
<211> 384
<212> PRT
<213> ospC Chimera

<400> 56
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
85 90 95
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
100 105 110
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
115 120 125
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
130 135 140
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
145 150 155 160
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
165 170 175
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys
180 185 190
Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro
195 200 205
Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile
210 215 220

Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 225 230 235 240
 Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys
 245 250 255
 Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile
 260 265 270
 Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val
 275 280 285
 Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys
 290 295 300
 Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly
 305 310 315 320
 Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr
 325 330 335
 His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys
 340 345 350
 Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser
 355 360 365
 Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 370 375 380

<210> 57
 <211> 1161
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1161)

<400> 57
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 Met Cys Ser Asn Ser Gly Lys Gly Asp Ser Ala Ser Thr Asn Pro
 1 5 10 15
 gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa 96
 Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act 144
 Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45
 ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa 192
 Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
 50 55 60
 ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 240
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
 65 70 75 80
 ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
 85 90 95
 agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct 336
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
 100 105 110

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala 115 120 125	384
gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile 130 135 140	432
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat Leu Lys Thr His Ala Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp 145 150 155 160	480
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu 165 170 175	528
act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro 180 185 190	576
aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr 195 200 205	624
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys 210 215 220	672
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu 225 230 235 240	720
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys 245 250 255	768
ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser 260 265 270	816
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu 275 280 285	864
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys 290 295 300	912
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu 305 310 315 320	960
ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu 325 330 335	1008

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta	1056
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu	
340	345
355	360
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa	1104
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys	
370	375
380	
aaa cct taa	1152
Lys Pro *	
385	
<210> 58	
<211> 386	
<212> PRT	
<213> ospC Chimera	
<400> 58	
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro	
1 5 10 15	
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
35 40 45	
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys	
50 55 60	
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser	
65 70 75 80	
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu	
85 90 95	
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala	
100 105 110	
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala	
115 120 125	
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile	
130 135 140	
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp	
145 150 155 160	
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu	
165 170 175	
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro	
180 185 190	
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
195 200 205	
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
210 215 220	
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
225 230 235 240	
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys	
245 250 255	
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser	
260 265 270	
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu	
275 280 285	

<210> 59
<211> 1197
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1197)

<400> 59
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 130 135 140	432
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 145 150 155 160	480
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 165 170 175	528
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 180 185 190	576
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 195 200 205	624
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp 210 215 220	672
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn 225 230 235 240	720
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu 245 250 255	768
gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala 260 265 270	816
aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag Lys Ala Ile Gly Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu 275 280 285	864
gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn 290 295 300	912
tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys 305 310 315 320	960
gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys 325 330 335	1008
tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp 340 345 350	1056
aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly 355 360 365	1104

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
 370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

<210> 60
<211> 398
<212> PRT
<213> ospC Chimera

<400> 60
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1 5 10 15
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
 85 90 95
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
 100 105 110
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
 130 135 140
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
 145 150 155 160
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
 165 170 175
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
 180 185 190
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp Gly
 210 215 220
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 225 230 235 240
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 245 250 255
 Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys
 260 265 270
 Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala
 275 280 285
 Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu
 290 295 300
 Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala
 305 310 315 320
 Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu
 325 330 335

Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn
 340 345 350
 Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala
 355 360 365
 Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala
 370 375 380
 Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

<210> 61
<211> 1196
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1196)

<p><400> 61</p> <p>atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 1 5 10 15</p> <p>gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 20 25 30</p> <p>gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 35 40 45</p> <p>aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 50 55 60</p> <p>ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 65 70 75 80</p> <p>gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 85 90 95</p> <p>acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 100 105 110</p> <p>tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 115 120 125</p> <p>aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 130 135 140</p> <p>aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 145 150 155 160</p>	<p>48</p> <p>96</p> <p>144</p> <p>192</p> <p>240</p> <p>288</p> <p>336</p> <p>384</p> <p>432</p> <p>480</p>
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gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 165 170 175	528
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 180 185 190	576
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 195 200 205	624
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp 210 215 220	672
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn 225 230 235 240	720
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val Leu 245 250 255	768
gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala 260 265 270	816
act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc Thr Lys Ala Ile Gly Lys Ile Gln Gln Asn Gly Gly Leu Ala Val 275 280 285	864
gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser 290 295 300	912
aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu 305 310 315 320	960
aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys 325 330 335	1008
aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp 340 345 350	1056
gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys 355 360 365	1104
ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala 370 375 380	1152

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac	1196
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu	
385 390	395

<210> 62
<211> 397
<212> PRT
<213> ospC Chimera

<400> 62

Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ile	Gly	Cys	Ala		
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Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	Asp
						20				25			30		
Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn
						35				40			45		
Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu
						50				55			60		
Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala
						65				70			75		80
Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	Thr
						85				90			95		
Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser
						100				105			110		
Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys
						115				120			125		
Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys
						130				135			140		
Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala
						145				150			155		160
Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys	Thr	Asn	Gly	Thr	Lys	Thr	Lys	Gly
						165				170			175		
Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	Lys
						180				185			190		
Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro
						195				200			205		
Val	Val	Ala	Glu	Ser	Pro	Ala	Met	Val	Asn	Asn	Ser	Gly	Lys	Asp	Gly
						210				215			220		
Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu
						225				230			235		240
Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala
						245				250			255		
Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr
						260				265			270		
Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	Leu	Ala	Val	Glu
						275				280			285		
Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser	Lys
						290				295			300		
Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	Glu	Lys	Leu	Lys
						305				310			315		320
Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe	Thr	Lys	Lys
						325				330			335		
Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile	Glu	Asn	Val	Thr	Asp	Glu
						340				345			350		
Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp	Ala	Ala	Lys	Asp	Lys	Gly
						355				360			365		

Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys
 370 375 380
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390 395

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<213> ospC Chimera

<220>
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu 180 185 190	576
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr 195 200 205	624
agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser 210 215 220	672
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile 225 230 235 240	720
agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu 245 250 255	768
gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly 260 265 270	816
aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn 275 280 285	864
gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys 290 295 300	912
aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu 305 310 315 320	960
aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu 325 330 335	1008
cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys 340 345 350	1056
gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu 355 360 365	1104
gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu 370 375 380	1152
atg ctt act aat tca gtt aaa gag ctt aca agc Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser 385 390 395	1185

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<212> PRT
<213> ospC Chimera

<400> 64

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Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	Asp
						20			25					30	
Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn
						35			40					45	
Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu
						50			55					60	
Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ala
						65			70					80	
Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Ser	Leu	Asp	Asn	Glu
						85			90					95	
Ala	Asn	Arg	Asn	Glu	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser	Thr
						100			105					110	
Leu	Ile	Thr	Gln	Lys	Leu	Ser	Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu	Lys
						115			120					125	
Glu	Lys	Ile	Ala	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Ser	Thr	Lys
						130			135					140	
Leu	Lys	Asp	Asn	His	Ala	Gln	Leu	Gly	Ile	Gln	Gly	Val	Thr	Asp	Glu
						145			150					160	
Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Ala	Asn	Ala	Ala	Gly	Lys	Asp	Lys
						165			170					175	
Gly	Val	Glu	Glu	Leu	Glu	Lys	Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu	Ser
						180			185					190	
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser
						195			200					205	
Pro	Val	Val	His	Gly	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala
						210			215					220	
Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser
						225			230					240	
Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val
						245			250					255	
Glu	Thr	Leu	Leu	Thr	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys
						260			265					270	
Lys	Ile	Lys	Asn	Asp	Val	Ser	Leu	Asp	Asn	Glu	Ala	Asp	His	Asn	Gly
						275			280					285	
Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	Leu	Ile	Thr	Lys	Lys
						290			295					300	
Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys
						305			310					320	
Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu	His
						325			330					335	
Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn	Ala	Lys	Lys	Ala
						340			345					350	
Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala	Asp	Glu	Leu	Glu
						355			360					365	
Lys	Leu	Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met
						370			375					380	
Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser						
						385			390						

<210> 65
<211> 1184

<212> DNA
<213> ospC Chimera

<220>
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

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gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
          20           25           30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

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aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50          55          60

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ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt      240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
   65           70           75           80

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gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
          100           105           110

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acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125

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aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act    432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
   130          135          140

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aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145           150           155           160

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gaaaatgcaaaaacctattttaaaagcataatgcacgcgggtaaaat
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175

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aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
          180           185           190

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tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195 200 205

agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser 210 215 220	672
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile 225 230 235 240	720
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu 245 250 255	768
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile 260 265 270	816
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His 275 280 285	864
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr 290 295 300	912
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile 305 310 315 320	960
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly 325 330 335	1008
gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys 340 345 350	1056
aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu 355 360 365	1104
ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys 370 375 380	1152
gag atg ctt gct aat tca gtt aaa gag ctt ac Glu Met Leu Ala Asn Ser Val Lys Glu Leu 385 390	1184
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 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
 85 90 95
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
 100 105 110
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
 130 135 140
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
 145 150 155 160
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
 165 170 175
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
 210 215 220
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 225 230 235 240
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
 245 250 255
 Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
 260 265 270
 Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn
 275 280 285
 Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln
 290 295 300
 Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu
 305 310 315 320
 Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu
 325 330 335
 His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
 340 345 350
 Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
 355 360 365
 Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
 370 375 380
 Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390

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1 5 10 15	
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
65 70 75 80	
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn	
85 90 95	
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100 105 110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115 120 125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130 135 140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145 150 155 160	
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165 170 175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	
agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser	
210 215 220	

aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225 230 235 240	240
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245 250 255	255
gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att	816
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile	
260 265 270	270
ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac	864
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn	
275 280 285	285
aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa	912
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu	
290 295 300	300
aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca	960
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr	
305 310 315 320	320
gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat	1008
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His	
325 330 335	335
gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct	1056
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala	
340 345 350	350
att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa	1104
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355 360 365	365
aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr	
370 375 380	380
tta aaa aat gct gtt aaa gag ctt aca agt cc	1184
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser	
385 390	390
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Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
35 40 45	
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu	
50 55 60	

Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
 85 90 95
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
 100 105 110
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
 130 135 140
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
 145 150 155 160
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
 165 170 175
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr
 210 215 220
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 225 230 235 240
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
 245 250 255
 Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
 260 265 270
 Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr
 275 280 285
 Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys
 290 295 300
 Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala
 305 310 315 320
 Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala
 325 330 335
 Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile
 340 345 350
 Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys
 355 360 365
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 370 375 380
 Lys Asn Ala Val Lys Glu Leu Thr Ser
 385 390

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<220>
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 <222> (1)...(1209)

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 20 25 30	96
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 35 40 45	144
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 50 55 60	192
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu 65 70 75 80	240
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat Ala Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn 85 90 95	288
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser 100 105 110	336
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu 115 120 125	384
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr 130 135 140	432
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp 145 150 155 160	480
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat Glu Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp 165 170 175	528
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu 180 185 190	576
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr 195 200 205	624
agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr 210 215 220	672
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys 225 230 235 240	720
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu 245 250 255	768

gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys 260 265 270	816
ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser 275 280 285	864
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu 290 295 300	912
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys 305 310 315 320	960
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu 325 330 335	1008
ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu 340 345 350	1056
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu 355 360 365	1104
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr 370 375 380	1152
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys 385 390 395 400	1200
aaa cct taa Lys Pro *	1209

<210> 70
<211> 401
<212> PRT
<213> ospC Chimera

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Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
65 70 75 80

Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
 85 90 95
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
 100 105 110
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
 130 135 140
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
 145 150 155 160
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
 165 170 175
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
 210 215 220
 Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
 225 230 235 240
 Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
 245 250 255
 Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile
 260 265 270
 Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 275 280 285
 Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
 290 295 300
 Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys Asp
 305 310 315 320
 Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
 325 330 335
 Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
 340 345 350
 Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
 355 360 365
 Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
 370 375 380
 Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
 385 390 395 400
 Pro

<210> 71
 <211> 1179
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1179)

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 20 25 30	96
gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 35 40 45	144
aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val 50 55 60	192
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu 65 70 75 80	240
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala 85 90 95	288
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser 100 105 110	336
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys 115 120 125	384
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys 130 135 140	432
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp 145 150 155 160	480
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly 165 170 175	528
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys 180 185 190	576
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro 195 200 205	624
att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn 210 215 220	672
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys 225 230 235 240	720
aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu 245 250 255	768

act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa		816
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys		
260	265	270
ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca		864
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser		
275	280	285
tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata		912
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile		
290	295	300
agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct		960
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala		
305	310	315
aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca		1008
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr		
325	330	335
gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att		1056
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile		
340	345	350
tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag		1104
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys		
355	360	365
tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt		1152
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu		
370	375	380
act aat tca gtt aaa gag ctt aca agc		1179
Thr Asn Ser Val Lys Glu Leu Thr Ser		
385	390	
<210> 72		
<211> 392		
<212> PRT		
<213> ospC Chimera		
<400> 72		
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys Ala		
1 5 10 15		
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Ser Gly Lys Asp		
20 25 30		
Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn		
35 40 45		
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu		
50 55 60		
Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala		
65 70 75 80		
Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn		
85 90 95		
Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp		
100 105 110		

Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu
 115 120 125
 Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu
 130 135 140
 Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn
 145 150 155 160
 Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala
 165 170 175
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala
 180 185 190
 Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile
 195 200 205
 Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 210 215 220
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 225 230 235 240
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 245 250 255
 Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 260 265 270
 Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu
 275 280 285
 Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser
 290 295 300
 Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys
 305 310 315 320
 Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp
 325 330 335
 Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu
 340 345 350
 Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu
 355 360 365
 Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr
 370 375 380
 Asn Ser Val Lys Glu Leu Thr Ser
 385 390

<210> 73
 <211> 1178
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1178)

<400> 73
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt		192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val		
50	55	60
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt		240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu		
65	70	75
80		
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc		288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala		
85	90	95
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct		336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser		
100	105	110
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag		384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys		
115	120	125
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa		432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys		
130	135	140
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat		480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp		
145	150	155
160		
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt		528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly		
165	170	175
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa		576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys		
180	185	190
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct		624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro		
195	200	205
att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat		672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn		
210	215	220
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa		720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys		
225	230	235
240		
aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa		768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu		
245	250	255
act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa		816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys		
260	265	270

aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly 275 280 285	864
aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys 290 295 300	912
tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn 305 310 315 320	960
gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His 325 330 335	1008
gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala 340 345 350	1056
att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu 355 360 365	1104
aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met 370 375 380	1152
ctt gct aat tca gtt aaa gag ctt ac Leu Ala Asn Ser Val Lys Glu Leu 385 390	1178
<210> 74	
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<213> ospC Chimera	
<400> 74	
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Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp 20 25 30	
Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn 35 40 45	
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu 50 55 60	
Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala 65 70 75 80	
Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn 85 90 95	
Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp 100 105 110	
Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu 115 120 125	
Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu 130 135 140	
Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn 145 150 155 160	

Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala
 165 170 175
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala
 180 185 190
 Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile
 195 200 205
 Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 210 215 220
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 225 230 235 240
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr
 245 250 255
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 260 265 270
 Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr
 275 280 285
 Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu
 290 295 300
 Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala
 305 310 315 320
 Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala
 325 330 335
 Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile
 340 345 350
 Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys
 355 360 365
 Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu
 370 375 380
 Ala Asn Ser Val Lys Glu Leu
 385 390

<210> 75
 <211> 1178
 <212> DNA
 <213> ospC Chimera

 <220>
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 <222> (1)...(1178)

<400> 75
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 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

 aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu 65 70 75 80	240
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala 85 90 95	288
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser 100 105 110	336
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys 115 120 125	384
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys 130 135 140	432
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp 145 150 155 160	480
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly 165 170 175	528
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys 180 185 190	576
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro 195 200 205	624
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn 210 215 220	672
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys 225 230 235 240	720
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu 245 250 255	768
acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys 260 265 270	816
aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser 275 280 285	864
ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu 290 295 300	912

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag		960
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys		
305	310	315
320		
caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg		1008
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val		
325	330	335
ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta		1056
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu		
340	345	350
aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta		1104
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu		
355	360	365
ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa		1152
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys		
370	375	380
aat gct gtt aaa gag ctt aca agt cc		1178
Asn Ala Val Lys Glu Leu Thr Ser		
385	390	

<210> 76
<211> 391
<212> PRT
<213> ospC Chimera

<400> 76

Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala			
1	5	10	15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp			
20	25	30	
Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn			
35	40	45	
Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val Leu			
50	55	60	
Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala			
65	70	75	80
Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn			
85	90	95	
Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp			
100	105	110	
Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu			
115	120	125	
Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu			
130	135	140	
Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn			
145	150	155	160
Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala			
165	170	175	
Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala			
180	185	190	
Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile			
195	200	205	

Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser
 210 215 220
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 225 230 235 240
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 245 250 255
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 260 265 270
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 275 280 285
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 290 295 300
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
 305 310 315 320
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 325 330 335
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
 340 345 350
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 355 360 365
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
 370 375 380
 Ala Val Lys Glu Leu Thr Ser
 385 390

<210> 77
 <211> 1230
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1230)

<400> 77
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 100 105 110	336
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 115 120 125	384
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat Lys Glu Lys Ile Asp Ala Ala Lys Cys Ser Glu Thr Phe Thr Asn 130 135 140	432
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 145 150 155 160	480
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 165 170 175	528
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 180 185 190	576
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 195 200 205	624
cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser 210 215 220	672
ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro 225 230 235 240	720
aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu 245 250 255	768
ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu 260 265 270	816
tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac Ser Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn 275 280 285	864
gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser 290 295 300	912
aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys 305 310 315 320	960

<210> 78
<211> 408
<212> PRT
<213> ospC Chimera

Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn
 225 230 235 240
 Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu
 245 250 255
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser
 260 265 270
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu
 275 280 285
 Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys
 290 295 300
 Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys
 305 310 315 320
 Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu
 325 330 335
 Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn
 340 345 350
 Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala
 355 360 365
 Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala
 370 375 380
 Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val
 385 390 395 400
 Val Ala Glu Ser Pro Lys Lys Pro
 405

<210> 79
<211> 1209
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1209)

<400> 79
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 100 105 110	336
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 115 120 125	384
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 130 135 140	432
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 145 150 155 160	480
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act act aaa act aaa Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 165 170 175	528
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 180 185 190	576
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 195 200 205	624
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser 210 215 220	672
ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys 225 230 235 240	720
ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala 245 250 255	768
gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp 260 265 270	816
gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu 275 280 285	864
gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu 290 295 300	912
att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly 305 310 315 320	960
gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt	1008

Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe			
325	330	335	
act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt		1056	
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val			
340	345	350	
act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa		1104	
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys			
355	360	365	
act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac		1152	
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn			
370	375	380	
ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt		1200	
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu			
385	390	395	400
aca agc taa		1209	
Thr Ser *			

<210> 80
<211> 401
<212> PRT
<213> ospC Chimera

<400> 80		
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys Ala		
1 5 10 15		
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp		
20 25 30		
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn		
35 40 45		
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu		
50 55 60		
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala		
65 70 75 80		
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr		
85 90 95		
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser		
100 105 110		
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys		
115 120 125		
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys		
130 135 140		
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala		
145 150 155 160		
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly		
165 170 175		
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys		
180 185 190		
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro		
195 200 205		
Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly		
210 215 220		

Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
 225 230 235 240
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
 245 250 255
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu
 260 265 270
 Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp
 275 280 285
 Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile
 290 295 300
 Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu
 305 310 315 320
 Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
 325 330 335
 Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr
 340 345 350
 Asp Asp Asn Ala Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr
 355 360 365
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
 370 375 380
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
 385 390 395 400
 Ser

<210> 81
<211> 1205
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1205)

<400> 81
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 100 105 110	336
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 115 120 125	384
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat Lys Glu Lys Ile Asp Ala Ala Lys Cys Ser Glu Thr Phe Thr Asn 130 135 140	432
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 145 150 155 160	480
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 165 170 175	528
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 180 185 190	576
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 195 200 205	624
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser 210 215 220	672
gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys 225 230 235 240	720
ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala 245 250 255	768
gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp 260 265 270	816
gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly 275 280 285	864
tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr 290 295 300	912
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser 305 310 315 320	960

gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp 325 330 335	1008
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn 340 345 350	1056
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala 355 360 365	1104
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu 370 375 380	1152
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu 385 390 395 400	1200
ctt ac Leu	1205

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<210> 82  
<211> 400  
<212> PRT  
<213> ospC Chimera
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<400> 82
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
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 1
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
 85 90 95
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
 100 105 110
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
 130 135 140
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
 145 150 155 160
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
 165 170 175
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
 180 185 190
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly
 210 215 220

Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly
225					230					235				240	
Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val
				245					250				255		
Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu
			260				265					270			
Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	Leu
			275				280					285			
Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	Thr
		290			295						300				
Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	Glu
305					310					315				320	
Lys	Leu	Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe
				325					330				335		
Thr	Lys	Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile	Glu	Asn	Val
				340				345				350			
Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp	Ala	Ala	Lys
				355				360				365			
Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn
				370				375				380			
Leu	Ala	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu
					390					395				400	

<210> 83
<211> 1236
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1236)

<400> 83 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt agt aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys
 20 25 30

ggt ggg gat tct gca tct act aat cct gct gac gag tct gcg aaa ggg 144
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly
35 40 45

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cct aat ctt aca gaa ata agc aaa aaa att aca gat tct aat gca ttt      192
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
      50          55          60

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gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa 240
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
65 70 75 80

cct gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta 288
 Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
 85 90 95

gct gct tta aat aat cag aat gga tcg ttg tta gca gga gcc tat gca Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala 100 105 110	336
ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu 115 120 125	384
gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe 130 135 140	432
act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala 145 150 155 160	480
acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr 165 170 175	528
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gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala 245 250 255	768
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Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln	
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350	
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Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp	
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Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu	
370	375
380	
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Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr	
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35 40 45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Val
50 55 60
Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu Leu
65 70 75 80
Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Gly Leu Ala
85 90 95
Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
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Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu Glu
115 120 125
Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
130 135 140
Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala Thr
145 150 155 160
Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr Asp
165 170 175
Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly Leu
180 185 190
Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
195 200 205
Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn Asn
210 215 220
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
225 230 235 240

Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
245 250 255
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
260 265 270
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
275 280 285
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
290 295 300
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
305 310 315 320
Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
325 330 335
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
340 345 350
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
355 360 365
Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
370 375 380
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
385 390 395 400
Pro Val Val Ala Glu Ser Pro Lys Lys Pro
405 410

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Raymond J. Dattwyler, Gerald Steinost, Daniel Dykhuizen,
Benjamin J. Luft and Maria J. C. Gomes-Solecki

Title: GROUPS OF BORRELIA BURGDORFERI AND BORRELIA
AFZELII THAT CAUSE LYME DISEASE IN HUMANS

TRANSMITTAL OF SEQUENCE LISTING IN COMPUTER READABLE FORM
IN COMPLIANCE WITH 37 C.F.R. §§1.821(e) AND (f)

Box Patent Application
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith is a copy of the "Sequence Listing" in computer readable form as required by 37 C.F.R. §1.821(e). As required by 37 C.F.R. §1.821(f), Applicant's Attorney hereby states that the content of the "Sequence Listing" in paper form and of the computer readable form of the "Sequence Listing" are the same.

Respectfully submitted,

HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

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Date: June 19, 2000